

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Bryce Tedeschi Examiner #: 78150 Date: 1/27/01  
 Art Unit: 1642 Phone Number 308-4823 Serial Number: 091389545  
 Mail Box and Bldg/Room Location: CM1/9<sup>TH</sup> Floor, room Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Composition and Methods for the prevention & treatment of ...

Inventors (please provide full names): Culin R. Dunstan

Earliest Priority Filing Date: 9/3/99

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

① Amino Acid Residues 186-401 in SEQ. ID #2

② Amino Acid Residues 22-194 in SEQ. ID #2

BEST AVAILABLE COPY

\*\*\*\*\*  
 SE ONLY

## Type of Search

## Vendors and cost where applicable

Location: <u>308-4499</u>	NA Sequence (#) _____	CTN _____
Searcher Picked Up: _____	AA Sequence (#) _____	Dialog _____
Completed: <u>1/27/01</u>	Structure (#) _____	Questel/Orbit _____
Searcher Prep & Review Time: _____	Bibliographic _____	Dr.Link _____
Clerical Prep Time: _____	Litigation _____	Lexis/Nexis _____
Online Time: _____	Fulltext _____	Sequence Systems _____
	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2001, 11:24:32 ; Search time 41.41 Seconds

(without alignments)  
489.664 Million cell updates/sec

Title: US-09-389-545-2\_COPY\_22\_194

Perfect score: 993

Sequence: 1 ETLPPKYLHNDPETHQLLC.....QKGNATHDNYCSGNREATOK 173

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 405 summaries

Database :

SPTREMBL\_15.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	993	100.0	401	11	008712 mus musculu
2	936	94.3	401	11	008727 mus musculu
3	887	89.3	372	4	Q90HP4 ratu
4	887	89.3	401	4	000300 mus sapien
5	420	42.3	300	4	095407 mus sapien
6	390.5	39.3	302	13	Q9PUS0 mus sapien
7	300	30.2	459	11	062327 mus sapien
8	298	30.0	439	4	Q16042 mus sapien
9	287.5	28.0	482	11	088734 mus sapien
10	278	28.0	655	4	075509 mus sapien
11	243.5	24.5	616	4	Q9Y606 mus sapien
12	239	24.1	625	11	035305 mus sapien
13	210.5	21.2	348	12	057112 variola vir
14	210.5	21.2	348	12	085407 variola vir
15	209.5	21.1	349	12	057110 variola vir
16	209.5	21.1	349	12	057111 variola vir
17	209.5	21.1	349	12	089098 variola vir
18	208.5	21.0	349	12	057099 monkeypox v
19	208.5	21.0	349	12	Q89118 variola vir

20	208	20.9	349	12	057284 monkeypox v
21	208	20.9	349	12	057098 monkeypox v
22	206.5	20.8	349	12	057281 monkeypox v
23	206.5	20.8	349	12	057100 monkeypox v
24	206.5	20.8	349	12	057101 monkeypox v
25	206.5	20.8	349	12	057102 monkeypox v
26	204	20.5	283	4	Q92956 mus sapien
27	204	20.5	283	4	Q92956 mus sapien
28	204	20.5	349	12	057097 monkeypox v
29	203	20.4	348	12	057277 monkeypox v
30	203	20.4	348	12	057103 monkeypox v
31	203	20.4	348	12	057108 monkeypox v
32	202.5	20.4	349	12	057109 monkeypox v
33	202.5	20.4	350	12	057116 monkeypox v
34	202	20.3	355	12	085308 monkeypox v
35	201.5	20.3	316	12	057092 monkeypox v
36	201	20.2	320	12	057091 monkeypox v
37	201	20.2	320	12	057300 monkeypox v
38	200	20.1	349	12	057305 monkeypox v
39	197	19.8	360	12	057118 monkeypox v
40	196	19.7	351	12	057117 monkeypox v
41	195.5	19.7	326	12	057120 monkeypox v
42	195.5	19.7	326	12	057122 monkeypox v
43	194	19.5	350	12	057123 monkeypox v
44	193.5	19.5	320	12	057079 monkeypox v
45	193.5	19.5	351	12	073559 monkeypox v

## ALIGNMENTS

RESULT 1  
ID 008712 PRELIMINARY: PRT: 401 AA.  
AC 008712; 070202;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE OSTEOCLASTOGENESIS INHIBITORY FACTOR,  
DE (OCIF).  
GN TNFRSF11B OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi,  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=KIDNEY;  
RX MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shuman G.,  
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patel W.,  
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
RA Suggs S., Boyle W.J.,  
RA "Osteoprotegerin: a novel secreted protein involved in the regulation  
of bone density.";  
RT Cell 89:309-319(1997).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/Ola, AND NIH SWISS;  
RX MEDLINE=96382527; PubMed=9714833;  
RA Higashio K., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morin J.P.,  
RA Mizuno A.,  
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OPG)  
gene and its expression in embryogenesis.";  
RL Gene 215:339-343(1998).  
-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF BONE  
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND  
 CC PLACENTA. NOT DETECTED IN SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
 CC 15 TO DAY 17.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: U94331; AAB53708.1; -.  
 DR EMBL: AB013898; BAA28269.1; -.  
 DR EMBL: AB013903; BAA33388.1; -.  
 DR EMBL: AB013899; BAA33388.1; JOINED.  
 DR EMBL: AB013900; BAA33388.1; JOINED.  
 DR EMBL: AB013901; BAA33388.1; JOINED.  
 DR EMBL: AB013902; BAA33388.1; JOINED.  
 DR HSSP: P25942; ICDF.  
 DR MGD: MGI:109587; Opg.  
 DR INTERPRO: IPR000488; -.  
 DR INTERPRO: IPR001368; -.  
 DR PFAM: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 DR Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 201 4 X TNFR-CYS.  
 FT REPEAT 23 63 TNFR-CYS 1.  
 FT REPEAT 64 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 98 POTENTIAL.  
 FT CARBOHYD 165 165 POTENTIAL.  
 FT CARBOHYD 178 178 POTENTIAL.  
 FT CARBOHYD 289 289 POTENTIAL.  
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).  
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).  
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).  
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).  
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).  
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 100.0%; Score 993; DB 11; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-96;  
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETLPPKYLHVPETGHOILCDKCAPGYTLKQCHTVRRKTLCPDPHSYDSDSWHTSDECV 60  
 DB 22 ETLPPKYLHVPETGHOILCDKCAPGYTLKQCHTVRRKTLCPDPHSYDSDSWHTSDECV 81  
 QY 61 YCSVYCKELQSVKQECNTHNRVCEGEGRYLLEIEFLCKHRSCTPPSGGVVQAGTPERNVY 120  
 DB 82 YCSVYCKELQSVKQECNTHNRVCEGEGRYLLEIEFLCKHRSCTPPSGGVVQAGTPERNVY 141  
 QY 121 CKKCPDFFSGEETSSKAPCIKHTKCSFGLLLLOKGNATHNVCSSGNREAROK 173  
 DB 142 CKKCPDFFSGEETSSKAPCIKHTKCSFGLLLLOKGNATHNVCSSGNREAROK 194

RESULT 2  
 ID 008727 PRELIMINARY; PRT; 401 AA.  
 DT 01-JUL-1997 (Tremblrel. 04, Created)  
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OSIF).  
 OS TNFRSF11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINE;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Liethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimizu J.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan W.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Farpley J., Derby P., Lee R.,  
 RA Sugis S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density.";  
 RL Cell 89:309-319(1997).  
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF HEAVILY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: U94330; AAB53707.1; -.  
 DR HSSP: P25942; ICDF.  
 DR INTERPRO: IPR001368; -.  
 DR PFAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 DR Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 201 4 X TNFR-CYS.  
 FT REPEAT 23 63 TNFR-CYS 1.  
 FT REPEAT 64 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 98 POTENTIAL.  
 FT CARBOHYD 165 165 POTENTIAL.  
 FT CARBOHYD 178 178 POTENTIAL.  
 FT CARBOHYD 289 289 POTENTIAL.  
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;

Query Match 94.3%; Score 936; DB 11; Length 401;  
 Best Local Similarity 93.6%; Pred. No. 3.4e-90;  
 Matches 161; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ETLPPKYLHVPETGHOILCDKCAPGYTLKQCHTVRRKTLCPDPHSYDSDSWHTSDECV 60  
 DB 22 ETLPPKYLHVPETGHOILCDKCAPGYTLKQCHTVRRKTLCPDPHSYDSDSWHTSDECV 81  
 QY 61 YCSVYCKELQSVKQECNTHNRVCEGEGRYLLEIEFLCKHRSCTPPSGGVVQAGTPERNVY 120  
 DB 82 YCSVYCKELQSVKQECNTHNRVCEGEGRYLLEIEFLCKHRSCTPPSGGVVQAGTPERNVY 141  
 QY 121 CKKCPDFFSGEETSSKAPCIKHTKCSFGLLLLOKGNATHNVCSSGNREAROK 173  
 DB 142 CKKCPDFFSGEETSSKAPCIKHTKCSFGLLLLOKGNATHNVCSSGNREAROK 194

DB 22 ETPPPKYLHYDEPETHGOLLDCKCAPGTYLKOHCTVRRKTLVCVPCDPDYSTDMSHTSDECV 81  
 QY 61 YCSPVCKELQSVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPSSGVVQAGTPERNIV 120  
 DB 82 YCSPVCKELQTVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPGLGVQAGTPERNIV 141  
 QY 121 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 172  
 DB 142 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 193

RESULT 3  
 Q9UHP4 PRELIMINARY: PRT: 372 AA.

Q9UHP4: 01-MAY-2000 (TREMBLREL. 13, Created)  
 01-MAY-2000 (TREMBLREL. 13, Last sequence update)  
 01-OCT-2000 (TREMBLREL. 15, Last annotation update)  
 OSTROPROTEGERIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;  
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens."  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 31:680-684(1999).  
 DR EMBL: AF134187; AAF20168.1; -  
 DR HSSP: P25942; 1CDF.  
 DR INTERPRO: IPR001368; -  
 DR PFAM: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS0050; TNFR\_NGFR\_2; 2.  
 FT NON\_TER 1  
 FT SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 89.3%; Score 887; DB 4; Length 372;  
 Best Local Similarity 87.3%; Pred. No. 4.3e-85;  
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

DB 1 ETPPPKYLHYDEPETHGOLLDCKCAPGTYLKOHCTVRRKTLVCVPCDPDYSTDMSHTSDECV 60  
 1 ETPPPKYLHYDEPETHGOLLDCKCAPGTYLKOHCTVRRKTLVCVPCDPDYSTDMSHTSDECV 60  
 DB 61 YCSPVCKELQSVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPSSGVVQAGTPERNIV 120  
 61 YCSPVCKELQSVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPSSGVVQAGTPERNIV 120  
 DB 61 YCSPVCKELQTVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPGLGVQAGTPERNIV 141  
 61 YCSPVCKELQTVKQECNRTNHNRYCECEBGRYLEIEFCLKHSRCPGLGVQAGTPERNIV 141  
 QY 121 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 173  
 121 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 173  
 DB 121 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 193  
 121 CKKCPDGFSSGSETSSKAPCIKHTNCSFTGLLLIÖKGNATHDVCNCRATQ 193

RESULT 4  
 Q9UHP4 PRELIMINARY: PRT: 401 AA.

Q9UHP4: 01-MAY-2000 (TREMBLREL. 04, Created)  
 01-MAY-2000 (TREMBLREL. 04, Last sequence update)  
 01-OCT-2000 (TREMBLREL. 15, Last annotation update)  
 OSTROPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).  
 GN TNFRSF11B OR OPG OR OCIF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;

RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang N.S.,  
 RA Luehry R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density."  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG FIBROBLAST;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 RA Tsuda E., Morinaga T., Higashio K.;  
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 osteoclastogenesis in vitro."  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 RT "Cloning and Characterization of the gene encoding human  
 osteoprotegerin/osteoclastogenesis-inhibitory factor."  
 RL Eur. J. Biochem. 254:685-691(1998).  
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,  
 KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
 A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN  
 THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: AB008822; BAA32076.1; -  
 DR EMBL: AB008821; BAA32076.1; JOINED.  
 DR EMBL: U94332; AAB53709.1; -  
 DR HSSP: P25942; 1CDF.  
 DR MIM: 602643; -  
 DR INTERPRO: IPR001368; -  
 DR PFAM: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS0050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1  
 FT CHAIN 21  
 FT DOMAIN 22 401  
 FT REPEAT 23 183  
 FT REPEAT 23 63  
 FT REPEAT 23 106  
 FT REPEAT 107 143  
 FT REPEAT 144 201  
 FT DOMAIN 306 365  
 FT DISULFD 41 54  
 FT DISULFD 44 62  
 FT DISULFD 65 80  
 FT DISULFD 83 97  
 FT DISULFD 87 105  
 FT DISULFD 118 142  
 FT DISULFD 145 160  
 FT CARBOHYD 98 98  
 FT CARBOHYD 152 152  
 FT CARBOHYD 165 165  
 FT CARBOHYD 178 178



062327  
ID 062327 PRELIMINARY: PRT: 459 AA.  
AC 062327:  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOB:  
RX MEDLINE=95178848; PubMed=7873884;  
POVELL E.E., WICKER L.S., PETERSON L.B., TODD J.A.;  
"Allelic variation of the type 2 tumor necrosis factor receptor  
gene.";  
RL Mamm. Genome 5:726-727(1994).  
DR EMBL: X76401; CA53981.1; -;  
DR HSSP: P19438; INCF.  
DR INTERPRO: IPR001368; -;  
DR PFAM: PF00020; TNFR\_C6; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
FT NON\_TER 1 1  
FT VARIANT 87 87 S -> T.  
FT VARIANT 93 93 T -> I.  
FT VARIANT 268 268 F -> I.  
FT VARIANT 345 345 S -> F.  
FT VARIANT 421 421 Y -> C.  
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 30.2%; Score 300; DB 11; Length 459;  
Best Local Similarity 35.2%; Pred. No. 1.4e-23;  
Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;

OY 10 YDPETGH-----QILCDKCAPGYTLKOHCTVRRKTLCPVPCDHSYTDSSMHTS 56  
DB 17 YKPEPGYECQISOEYDRKRAQMCCKCPGQYVKKHCKNTSDTVACDCEASMYTWMNV 76  
OY 57 DECVYSPYCKELQSVKQECNRTNHRVCECEGRYLEIEF-----CLKHRSPPGSGV 109  
DB 77 RFTCLSSSSCSSTQDYETRACTKQONRVCACEAGRYCALKTHSGSCGRCRLSKCGPGRV 136  
OY 110 VQAGPERNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGILLIOKGNATHDNVCS 165  
DB 137 ASSRAPNGNVLCACAPGTFSDTSTSDVCRPHRIS---ILAIIPGNASTDAVCA 188  
RESULT 8  
ID 016042 PRELIMINARY: PRT: 439 AA.  
AC 016042:  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-JAN-1999 (TREMblrel. 09, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91370690; PubMed=1966549;  
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,  
Brockhaus M., Lesliener W.;  
"Two human TNF receptors have similar extracellular, but distinct  
intracellular, domain sequences.";  
RL CytoKine 2:231-237(1990).  
DR EMBL: S63368; AAB19824.1; -;  
DR HSSP: P25942; ICDP.

DR INTERPRO: IPR001368; -;  
DR PFAM: PF00020; TNFR\_C6; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
DR PRODOM: PD000771; -; 1.  
SQ SEQUENCE 439 AA; 46090 MW; F6CBEB329C67FF6 CRC64;

Query Match 30.0%; Score 298; DB 4; Length 439;  
Best Local Similarity 35.6%; Pred. No. 2.2e-23;  
Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;

OY 10 YDPETGH-----QILCDKCAPGYTLKOHCTVRRKTLCPVPCDHSYTDSSMHTS 57  
DB 10 YKPEPGYECQISOEYDRKRAQMCCKCPGQYVKKHCKNTSDTVACDCEASMYTWMNV 69  
OY 58 DECVYSPYCKELQSVKQECNRTNHRVCECEGRYLEIEF-----EFLKHSPPGSGV 111  
DB 70 ECLSGSRCSSTQDYETRACTKQONRVCACEAGRYCALKTHSGSCGRCRLSKCGPGRV 129  
OY 112 AGTPERNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGILLIOKGNATHDNVCS 165  
DB 130 PETERSDVYCKPCAPGTFSDTSTSDVCRPHRIS---ILAIIPGNASTDAVCA 174

## RESULT 9

ID 088734 PRELIMINARY: PRT: 482 AA.

AC 088734:  
DT 01-NOV-1998 (TREMblrel. 08, Created)  
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
DE P80 TNF-ALPHA RECEPTOR.  
GN TNFR2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hurtle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
"The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure,  
RT Characterization of the two Transcripts.";  
RL Genomics 0:0-0(0).

DR EMBL: Y14619; CAAT74969.1; -;  
DR EMBL: Y14620; CAAT74969.1; JOINED.  
DR EMBL: Y14621; CAAT74969.1; JOINED.  
DR EMBL: Y14622; CAAT74969.1; JOINED.  
DR EMBL: Y14623; CAAT74969.1; JOINED.  
DR EMBL: Y14679; CAAT74969.1; JOINED.  
DR HSSP: P19438; INCF.  
DR INTERPRO: IPR001368; -;  
DR PFAM: PF00020; TNFR\_C6; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
DR PRODOM: PD000771; -; 1.  
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 29.0%; Score 287.5; DB 11; Length 482;  
Best Local Similarity 33.9%; Pred. No. 3.1e-22;  
Matches 62; Conservative 17; Mismatches 73; Indels 31; Gaps 4;

OY 10 YDPETGH-----QILCDKCAPGYTLKOHCTVRRKTLCPVPCDHSYTDSSMHTS 49  
DB 32 YKPEPGYECQISOEYDRKRAQMCCKCPGQYVKKHCKNTSDTVACDCEASMYTWMNV 91  
OY 50 TDSWHTSECVYSPYCKELQSVKQECNRTNHRVCECEGRYLEIEF-----CLKHRS 102  
DB 92 TQVWNPFTCLSSCSSTQDYETRACTKQONRVCACEAGRYCALKTHSGSCGRCRLSK 151  
OY 103 CPPGSGVYVQAGTPERNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGILLIOKGNATH 162

[illegible][illegible]



AC	03JAN1998 (TREMblrel_05_Created)
DT	01-JAN-1998 (TREMblrel_05_Last sequence update)
DT	01-OCT-2000 (TREMblrel_15_Last annotation update)
DE	RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
DE	INDUCED CYTOKINE RECEPTOR) (RANK).
GN	TNFRSF1A OR RANK.
OS	Mus musculus (Mouse)..
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX	NCHI_TaxID=10090;
RM	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER EPITHELIUM:
RX	MEDLINE=96032977; PubMed=93671155;
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
RL	Nature 390:175-179(1997).
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR	EMBL; AF019046; AAB86810.1; -
DR	HSSP; P25942; ICDF.
DR	MCD; MG1:J314891; Tnfifsfla.
DR	INTERPRO; IPRO00561; -
DR	INTERPRO; IPR001368; -
DR	Pfam; PF00020; TNFR_cg.3.
DR	PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_1.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00050; TNFR_NGFR.2; 1.
DR	PRODOM; PD000771; -; 1.
KW	Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT	SIGNAL 1 30
FT	CHAIN 31 625
FT	DOMAIN 31 214
FT	TRANSMEM 215 235
FT	DOMAIN 236 625
FT	DOMAIN 34 196
FT	REPEAT 34 70
FT	REPEAT 71 114
FT	REPEAT 115 153
FT	REPEAT 154 196
FT	DISULFID 35 47
FT	DISULFID 48 61
FT	DISULFID 51 69
FT	DISULFID 72 87
FT	DISULFID 93 113
FT	DISULFID 115 125
FT	DISULFID 127 134
FT	DISULFID 128 152
FT	DISULFID 155 170
FT	DISULFID 176 195
FT	CARBOHYD 106 106
FT	CARBOHYD 175 175
SE	SEQUENCE 625 AA; 66621 MW; F8C1872E9511D08 CRC64;
SE	N-LINKED (GLCNAC... ) (POTENTIAL).
SE	N-LINKED (GLCNAC... ) (POTENTIAL).
SE	F8C1872E9511D08 CRC64;

	Query Match	Score 239	DB 11	Length 625
	Best Local Similarity	33.9%	Pred. No. 4.7e-17	
	Matches 59	Conservative 21	Mismatches 82	Indels 12; Gaps 7
Oy	1	ELTLP--KYLHNDPETHOILCDKAPGYULQONCHVRRRKTKLRPCRDHSYDTSMTWSTDE	58	
		: :		
Dd	30	QVTPRCOTDERNVE-HLGR--CCSRCEPKXYLLSKCPTSDSVCLPCGPRDEIYDTWNNEEDK	86	
		: :		
Oy	59	CYYCSFVC---KELOSVKOEKNRTHNRVCECEBGR--LEIEFLKLNHSCRPDSGGVLYAG	113	
		: :		
Dd	87	CL-LHKVCAGAKALVAIV-DPGNNHTAARRCACATAGYHMNSDCESCRRENTCAIDFGAQNHPL	144	
		: :		
Oy	114	TPERNYVCKKKCPDGFFSGFTSSKAPCIKITIKNSTPDLILLIQGNATHDWVCSGN	167	

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Db      145 QLNKDVCTPCLLGGFSDVFSSTDKCXPMNTNCTLGKGLEAHQGTESDVCSSS    198  
RESULT   13  
057112 ID 057112 PRELIMINARY; PRT; 348 AA.  
AC       057112:  
DT       01-JUN-1998 (TREMBLrel_06, Created)  
DT       01-JUN-1998 (TREMBLrel_06, Last sequence update)  
DT       01-OCT-2000 (TREMBLrel_15, Last annotation update)  
DE       TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.  
GN       CRMB.  
OS       Variola virus.  
OC       Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinæ;  
OX       Orthopoxvirus.  
NCBI__taxid=10255;  
RN       [1]  
RP       SEQUENCE FROM N.A.  
RC       STRAIN='WHITEPOX' CHIMP 9-2 (CH9-2);  
RL       Loparev V.N., Parsons J.M., Esposto J.J.;  
RA       Submitted (FEB-1997) to the EMBL/GenBank/DDBB databases.  
RR       EMBL; U08151; AAB94376.1; -.  
DR       HSP; P25942; ICDF.  
DR       INTERPRO: IPR001368; -.  
DR       PFAM; PF00020; TNFR_C6; 2.  
DR       PROSITE; PS00652; TNFR_NGFR_1; 2.  
DR       PROSITE; PSS0050; TNFR_NGFR_2; 2.  
DR       PRODOL; PD000771; -; 1.  
SQ       SEQUENCE 348 AA; 38041 MW; 92D333794FC373E3 CRC64;
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Query Match Similarity      21.2%; Score 210.5; DB 12; Length 348;
Best Local Similarity      30.0%; Pred. No. 2,6e-14;
Matches      48; Conservative      19; Mismatches      76; Indels      17; Nips
Oy      10 YDPETG-----HQLCDKCAFGTYLKHQCTVARKRTLGVPCPDHSTYDSMHTSDFV 60
Db      24 YTPPMGKCKDTEYKRHHNLCLCLSPGTYASRLCDSKSTNTQCTPCGSGTFSRNHNP... 60
Oy      61 YSPVCKELQSVKQCCNRTFNHNVCCCEERYLEI-----ECLKHKRSPPSGVQAQT 114
Db      84 SCNGRCNSNQVETRSCNTTHNRICCCSPGYLLKGGSSCKACVSTQKGIYGV-VSGHT 142
Oy      115 PERNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQ 154
Db      143 SVGDVICSPCGRGTYSHYVSSADKEPVEN-NTFNIVDE 181

RESULT      14
ID      085407
NC      085407.      PRELIMINARY;      PRT;      348 AA.
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE      HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN      G2R OR CRM8.
OS      Variola virus.
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxviri...
OC      Orthopoxvirus.
OX      NCBI_Taxid=10255;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BANGLADESH-1975;
RX      MEDLINE=94088747; PubMed=8264798;
RA      Messing R.F., Esposito J.J., Liu L.I., Qi J., Utterback T.R.,
RA      Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.;
RT      "Potential virulence determinants in terminal regions of variola
RT      smallpox virus genome."
RL      Nature 366:748-751(1993).
RN      [2]
RP      SEQUENCE FROM N.A.

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JC STRAIN='WHITEPOX/CHIMP 9-4 (CH9-4);  
 RA Loparev V.N., Parsons J.M., Esposito J.J.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L22579; AAB60933.1; -;  
 DR EMBL: U88152; AAB94377.1; -;  
 DR HSSP: P25942; ICDF.  
 DR INTERPRO: IPR001368; -;  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 SO SEQUENCE 348 AA; 38075 MW; A9BE85AP94AB5369 CRC64;

Query Match 21.1%; Score 210.5; DB 12; Length 348;  
 Best Local Similarity 30.0%; Pred. No. 2.6e-14;  
 Matches 48; Conservative 19; Mismatches 76; Indels 17; Gaps 4;

QY 10 YDPETG-----HOLLCDKCAPGYLKQHCYVRRKTLCPGPDHSTDSWHTSDECV 60  
 DB 24 YTPNGKCKDTEYKRHNLCCLSCPGTYASRLCDKSTNTQCTPCGSGFTSRNNHLPACL 83  
 QY 61 YCSPVCKELQSVKQECNTHNRVCECEGRYLEI-----EFCCLKHRSCPPGSGVQAGT 114  
 DB 84 SCNGRCNSNOVETRSCNTHNRICECSPGYCYCLKGSSGCRACVSYQTCGIGYG-VSGHT 142  
 QY 115 PERNTVCKKCPDGFSGETSSKAPCIKHTNCTFGLLIQ 154  
 DB 143 SVGDVICSPCGFGTYSHTVSSADKCEVPN-NTFNVIDVE 181

RESULT 15  
 ID 057110 PRELIMINARY; PRT; 349 AA.  
 AC 057110:  
 DT 01-JUN-1998 (Tremblrel. 06, last sequence update)  
 DT 01-JUN-1998 (Tremblrel. 06, last sequence update)  
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.  
 GN CRMB.  
 OS Variola virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MAJOR, CONGO-1970 (CNG-70);  
 RA Loparev V.N., Parsons J.M., Esposito J.J.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U88147; AAB94372.1; -;  
 DR HSSP: P25942; ICDF.  
 DR INTERPRO: IPR001368; -;  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 SO SEQUENCE 349 AA; 38273 MW; 2987FF00CD4824F5 CRC64;

Query Match 21.1%; Score 209.5; DB 12; Length 349;  
 Best Local Similarity 30.0%; Pred. No. 3.3e-14;  
 Matches 48; Conservative 19; Mismatches 76; Indels 17; Gaps 4;

QY 10 YDPETG-----HOLLCDKCAPGYLKQHCYVRRKTLCPGPDHSTDSWHTSDECV 60  
 DB 25 YTPNGKCKDTEYKRHNLCCLSCPGTYASRLCDKSTNTQCTPCGSGFTSRNNHLPACL 84  
 QY 61 YCSPVCKELQSVKQECNTHNRVCECEGRYLEI-----EFCCLKHRSCPPGSGVQAGT 114  
 DB 85 SCNGRCNSNOVETRSCNTHNRICECSPGYCYCLKGSSGCRACVSYQTCGIGYG-VSGHT 143  
 QY 115 PERNTVCKKCPDGFSGETSSKAPCIKHTNCTFGLLIQ 154

DB 144 SVGDVICSPCGFGTYSHTVSSADKCEVPN-NTFNVIDVE 182

Search completed: January 27, 2001, 11:24:34  
 Job time: 116 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2001, 11:24:56 ; Search time 17.62 Seconds  
(without alignments)  
317.076 Million cell updates/sec

Title: US-09-389-545-2\_COPY\_22\_194  
Perfect score: 993  
Sequence: 1 ETLPKRLIHDPEGHQLJC.....QKGNATHDNCNGREATQR 173

String table: BIOSOM62  
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSprot\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	30.2	461	1	TNR2_HUMAN
2	297	29.9	474	1	TNR2_MOUSE
3	270	27.2	289	1	CD40_MOUSE
4	261	26.3	277	1	CD40_HUMAN
5	242.5	24.4	435	1	TNRC_HUMAN
6	227	22.9	329	1	CD40_BOVIN
7	226	22.8	325	1	VT2_SFVKA
8	210.5	21.2	349	1	VT2_MYXVL
9	210.5	21.2	349	1	VC22_VARY
10	203.5	20.5	415	1	TNRC_MOUSE
11	192.5	19.4	427	1	NGFR_HUMAN
12	188.5	19.0	425	1	NGFR_MOUSE
13	184	18.5	416	1	NGFR_CHICK
14	177	17.8	256	1	41BB_MOUSE
15	167	16.8	255	1	41BB_HUMAN
16	167	16.8	323	1	FASA_BOVIN
17	163	16.4	271	1	OX40_RAT
18	160	16.1	455	1	TNR1_MOUSE
19	159	16.0	454	1	TNR1_HUMAN
20	159	16.0	461	1	TNR1_PIG
21	152	15.3	272	1	OX40_MOUSE
22	148	14.9	461	1	TNR1_RAT
23	145	14.6	277	1	OX40_HUMAN
24	144.5	14.6	332	1	FASA_PIG
25	144	14.5	335	1	FASA_HUMAN
26	139	14.0	595	1	CD30_HUMAN
27	137.5	13.8	324	1	FASA_RAT
28	137	13.8	327	1	FASA_MOUSE
29	135	13.6	471	1	TNR1_BOVIN
30	125	12.6	1680	1	FUR2_DROME
31	118.5	11.9	1609	1	LMG1_HUMAN
32	115	11.6	417	1	WSL1_HUMAN
33	113.5	11.4	260	1	CD27_HUMAN

34	113.5	11.4	1607	1	LMG1_MOUSE
35	111	11.2	1955	1	ACR1_CHICK
36	109.5	11.0	250	1	CD27_MOUSE
37	109.5	11.0	667	1	TS11_GIALA
38	109	10.9	969	1	PAC4_HUMAN
39	108	10.9	713	1	TS44_GIALA
40	108	10.8	915	1	PAC6_MOUSE
41	107.5	10.8	722	1	DL1_MOUSE
42	107	10.8	1639	1	LMG1_DROME
43	106.5	10.7	3084	1	LM41_MOUSE
44	106	10.7	915	1	PAC6_RAT
45	105	10.6	1557	1	LM1L_CAEEL

## ALIGNMENTS

RESULT 1					
TNR2_HUMAN	STANDARD:	PRT:	461 AA.		
ID P20333:					
DT 01-FEB-1991 (Rel. 17, Created)					
DT 01-AUG-1991 (Rel. 19, Last sequence update)					
DT 01-OCT-2000 (Rel. 40, Last annotation update)					
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPL1) (P80) (TNF-R2) (P75) (CD120B) (ETANRECEP)					
GN TNR2_HUMAN					
OS Homo sapiens (Human)					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
LN [1]					
RA MEDLINE-90260639; PubMed-2160731;					
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;					
RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins."					
RL Science 248:1019-1023(1990).					
RN [2]					
RA MEDLINE-91045991; PubMed-2172983;					
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;					
RT "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor."					
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).					
RN [3]					
RA MEDLINE-96299745; PubMed-8661109;					
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S., Lepeslier D., Stallard B.J., Goeddel D.V., Desautave F.J., Brodeur G.M.;					
RT "Physical mapping and genomic structure of the human TNFR2 gene."					
RL Genomics 35:94-100(1996).					
RN [4]					
RA MEDLINE-90349572; PubMed-2166946;					
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;					
RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor."					
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).					
RN [5]					
RA MEDLINE-90110215; PubMed-2153136;					
RA Engelmann H., Novick D., Wallach D.;					
RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors."					
RL J. Biol. Chem. 265:1531-1536(1990).					
RN [6]					
RA MEDLINE-91056048; PubMed-2173696;					

RA Loetscher H., Schlaefer E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from H60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [7]  
 RP CHARACTERIZATION.  
 RP MEDLINE=93016040; PubMed=1328224;  
 RA Panica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE=99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBEL (IMMUNEX AND  
 CC WYETH-AVERT). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBEL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;  
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"  
 CC -1- DATABASE: NAME-Embel; NOTE=Clinical information on Embrel;  
 CC WWW=http://www.embrelinfo.com/".  
 CC -----  
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 CC -----  
 DR EMBL: M32315; AAA59929.1; -;  
 DR EMBL: M35857; AAA63262.1; -;  
 DR EMBL: U52165; AAC50622.1; -;  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -;  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.  
 DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MTM: 191191; -;  
 DR INTERPRO: IPR001368; -;  
 DR PFAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KM Receptor: Transmembrane; Glycoprotein; Repeat; Signal;  
 FT Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOSOLIC (POTENTIAL).  
 FT REPEAT 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 201 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.  
 FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 193 193 R -> P (IN REF. 4).  
 FT CONFLICT 141 141 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 196 196 A -> T (IN REF. 4).  
 FT CONFLICT 363 363  
 SQ SEQUENCE 461 AA; 48316 MM; 603B580CD67636F CRC64;  
 Query Match 30.2%; Score 300; DB 1; Length 461;  
 Best Local Similarity 35.6%; Pred. No. 5.1e-19;  
 Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;  
 QY 10 YDEPETH-----QLLDKCAPGTYLKHQCTVRKRLTVPDPHSYDWSHTSD 57  
 Db 32 YAPRPGSTCHLREYDQTAQMCSCSPGQHAKEVCFKTSDFVDCSDCEDSTYTQLMWVP 91  
 QY 58 ECVYCSGVCKELDSVQKOEKRNTRNRCVECEGRLEI-----EFLKHSCEPGSSVQ 111  
 Db 92 ECLSCGSRCSDDYETQACTREONRITCTCRPGWCAISKQEGRLCAPLKRCPGCVAR 151  
 QY 112 AGPERNTVCKKCPDDGFFSGETSSKAPCIRHTNCSFGLLLQGNATHDNVCS 165  
 Db 152 PGTETSDVCKPCAPGTFSTSTSDICRPHQICNVAVI-----PGNASKAVCT 201  
 RESULT 2  
 TNFR2\_MOUSE STANDARD; PRT; 474 AA.  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]

RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN-NOD:  
 RA Jacob C.O., Liu J.  
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.  
 RM [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=LIVER;  
 RA Kissonerghis M., Felloues R., Feldmann M., Chernaiovsky Y.;  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC -----  
 DR EMBL: M60469; AAA39752.1; -  
 DR EMBL: M59378; AAA40463.1; -  
 DR EMBL: U39488; AAA85021.1; -  
 DR EMBL: X87128; CAA60618.1; -  
 DR PIR: B38634; B38634.  
 DR HSSP: P19438; 1NCF.  
 DR MGD: MGI:1314883; TNFRSF1B.  
 DR INTERPRO: IPR001368; -  
 DR PIR: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00505; TNFR\_NGFR\_2; 3.  
 RA Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 259 288 POTENTIAL.  
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 203 4 X TNFR-CYS.  
 FT REPEAT 39 77 TNFR-CYS 1.  
 FT REPEAT 78 119 TNFR-CYS 2.  
 FT REPEAT 120 164 TNFR-CYS 3.  
 FT REPEAT 165 203 TNFR-CYS 4.  
 FT DISULFID 40 54 BY SIMILARITY.  
 FT DISULFID 55 68 BY SIMILARITY.  
 FT DISULFID 58 76 BY SIMILARITY.  
 FT DISULFID 79 94 BY SIMILARITY.  
 FT DISULFID 97 111 BY SIMILARITY.  
 FT DISULFID 101 119 BY SIMILARITY.  
 FT DISULFID 121 127 BY SIMILARITY.  
 FT DISULFID 136 145 BY SIMILARITY.  
 FT DISULFID 139 163 BY SIMILARITY.  
 FT DISULFID 166 181 BY SIMILARITY.  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 29.9%; Score 297; DB 1; Length 474;  
 Best Local Similarity 35.2%; Pred. No. 9.5e-19;  
 Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;

QY 10 YDPETGH-----QLLCKCAPGTYLKQHCYVRKRLTCLVCPDSDHSYTSWHTS 56  
 DB 32 YPREGYEQISQYEDYDKRAQKCAKCPGGYVYKFCNKTSDTVCADCEASMTYVWNOF 91  
 QY 57 DEVCYCSPYCKELQSVKQECNFTNHRVCECEGRLYLEIF-----CLKHSCPPGSGV 109  
 DB 92 RFLCSCSSCCTDYEIRACTGKQNRVCACEAGRYCALKTHSGSORQCMRLSKGPGGCV 151  
 QY 110 VQAGTPERTVCKKCPDGGFSGSETSSKAPCIHTNCSFTFGLLLIKGNATHDNVCS 165  
 DB 152 ASSRAPNGNVLCACAPGTFSTSTSDTSCVCRPHRIS-----TLAIPGNASTDAVCA 203

RESULT 3  
 CD40\_MOUSE STANDARD; PRT: 289 AA.  
 ID CD40\_MOUSE  
 AC P27512;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (M40).  
 GN TNFRSF5 OR CD40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:92105763; Pubmed=1370315;  
 RA Torres R.M., Clark E.A.;  
 RT "Differential increase of an alternatively polyadenylated mRNA  
 species of murine CD40 upon B lymphocyte activation."  
 RL J. Immunol. 148:620-626(1992).  
 RN [2]  
 RP REVISIONS.  
 RC STRAIN-BALB/C;  
 RA Torres R.M.;  
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=LIVER;  
 RX MEDLINE:93094586; Pubmed=1281194;  
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
 RA Howard M., Cockayne D.A.;  
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene."  
 RL J. Immunol. 149:3921-3926(1992).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL: M83312; AAB08705.1; -  
 DR EMBL: M94126; AAA37404.1; -  
 DR EMBL: M94129; AAA37404.1; JOINED.  
 DR EMBL: M94128; AAA37404.1; JOINED.  
 DR EMBL: M94127; AAA37404.1; JOINED.  
 DR PIR: A46476; A46476.  
 DR HSSP: P25942; 1CDF.  
 DR MGD: MGI:88336; TNFRSF5.  
 DR INTERPRO: IPR001368; -  
 DR PIR: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00505; TNFR\_NGFR\_2; 4.  
 RA Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 289 CD40L RECEPTOR.  
 FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 216 289 POTENTIAL.  
 FT DOMAIN 25 187 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 25 60 4 X TNFR-CYS.  
 FT REPEAT 61 103 TNFR-CYS 1.  
 FT REPEAT 104 144 TNFR-CYS 2.  
 FT REPEAT 145 187 TNFR-CYS 3.  
 FT CARBOHYD 153 153 TNFR-CYS 4.  
 SO SEQUENCE 289 AA; 32111 MW; C791CB62FEA574E CRC64;

Query Match 27.2%; Score 270; DB 1; Length 289;  
 Best Local Similarity 34.5%; Pred. No. 1,3e-16;  
 Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

DR PROSITE: P500652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: P550050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 3D-structure.

FT SIGNAL 1 19  
 FT CHAIN 20 277  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 277  
 FT DOMAIN 225 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180

SO SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

RESULT 4  
 CD40\_HUMAN STANDARD; PRT; 277 AA.  
 AC P25942;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40) (TUMOR NECROSIS FACTOR RECEPTOR 5).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89356608; PubMed=2475341;  
 RA Stamenkovic I., Clark E.A., Seed B.;  
 RT "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas";  
 RL EMO J. 8:1403-1410(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 24-144.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RA Bajorek J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 RN [3]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Wijmen H., Karsusas M., Hsu Y.-M.,  
 RT "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide: CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".

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CC EMBL: X60592; CAA43045.1;  
 CC PIR: S04460; S04460.  
 CC PDB: 1CDF; 01-APR-97.  
 CC MIM: 109535;  
 CC INTERPRO: IPR001368;  
 CC PFM: PF00020; TNFR\_C6; 4.

Query Match 26.3%; Score 261; DB 1; Length 277;  
 Best Local Similarity 33.9%; Pred. No. 7.2e-16;  
 Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

DR PROSITE: P500652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: P550050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 3D-structure.

FT SIGNAL 1 19  
 FT CHAIN 20 277  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 277  
 FT DOMAIN 225 187  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180

SO SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

RESULT 5  
 TNRC\_HUMAN STANDARD; PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DT LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
 GN LTRB OR TNFR OR TNFRSF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710(1994).  
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN

IMMUNE DEVELOPMENT.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC  
 DR EMBL: L04270; AAA36757.1; .  
 DR HSSP: P25942; 1CDF.  
 MIM: 600979; .  
 INTERPRO: IPR001368; .  
 PRAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; 3.  
 KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT DOMAIN 31 227  
 FT TRANSMEM 228 248  
 FT DOMAIN 249 435  
 FT DOMAIN 42 211  
 FT DOMAIN 42 81  
 FT REPEAT 82 124  
 FT REPEAT 125 168  
 FT REPEAT 169 211  
 FT REPEAT 43 58  
 FT DISULFID 59 72  
 FT DISULFID 62 80  
 FT DISULFID 83 98  
 FT DISULFID 101 116  
 FT DISULFID 104 124  
 FT DISULFID 126 132  
 FT DISULFID 139 148  
 FT DISULFID 142 167  
 FT DISULFID 170 185  
 FT CARBOHYD 40 40  
 FT CARBOHYD 177 177  
 SQ SEQUENCE 435 AA; 46709 MM; 624626E6022F656F CRC64;  
 Query Match 24.4%; Score 242.5; DB 1; Length 435;  
 Best Local Similarity 29.6%; Pred. No. 4.3e-14;  
 Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5;  
 Oy 9 HYDPEYHQLDCKAPGTYLKHQCTVRRKTLGVPCPDHSTYDSMHTDECVYCSFVCKE 68  
 Db 50 YEEPP--HRTCSRCPPPTVYSAKSRIDVYCATCAENSTNEHNNVLTICOLCRP-CDP 106  
 Oy 69 LOSVQK--ECNRTNHRVCECEGRY----LEIEFLKHRSCPSPG--GVVAGTPEERTV 120  
 Db 107 VMGLEELAPGTSKRRTGRCQRCQPGMFCAMALECTHCELLSDCPTEAEMLDEVCKGNH 166  
 Oy 121 CKKCPDGFSGETSSKAPCIKHTNCTFGLLIQLKGNATHDNVCSGNRE 169  
 Db 167 CVPCKAGHFQNTSPSARCOPHTRCENQGLVEAAGTAQSDTTCKNPLE 215  
 RESULT 6  
 CD40\_BOVIN STANDARD; PRT; 269 AA.  
 ID CD40\_BOVIN  
 AC Q28203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).  
 GN TNFRSF5 OR CD40.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97281252; PubMed-9135560;  
 RA Hirano A., Brown W.C., Estes D.M.;  
 RT "Cloning, expression and biological function of the bovine CD40  
 RT homologue: role in B-lymphocyte growth and differentiation in  
 RT cattle";  
 RL Immunology 90: 294-300(1997).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 DR EMBL: U57745; AAC48710.1; .  
 DR HSSP: P25942; 1CDF.  
 DR INTERPRO: IPR001368; .  
 DR PRAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; 1.  
 KM Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 269  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 269  
 FT DOMAIN 25 187  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 FT NON\_TER 269 269  
 SQ SEQUENCE 269 AA; 29983 MM; 746903F30F95F387 CRC64;  
 Query Match 22.9%; Score 227; DB 1; Length 269;  
 Best Local Similarity 33.1%; Pred. No. 6e-13;  
 Matches 57; Conservative 20; Mismatches 77; Indels 18; Gaps 5;  
 Oy 8 LHYDEPG-----HQLDCKAPGTYLKHQCTVRRKTLGVPCPDHSTYDSMHTSDEC 59  
 Db 18 VHSPEATGCGEGRYPVNSLDCDLPQGGKLVNDCETEVSCGSGKEFLSTNNREKVC 77  
 Oy 60 ---VYCSF--VEKELOSQVKECNRTNHRVCECEGRY----LEIEFLKHRSCPSPG 112  
 Db 78 HEHRKCNNGLRKDS---ESTLWDTICVCEGQHCSTHSCCTPHSLCLPFGVKOT 134  
 Oy 113 GTPERTNCKKCPDGFSGETSSKAPCIKHTNCTFGLLIQLKGNATHDNVNC 164  
 Db 135 ATGLDITVCECPGLGFGFSNVSAFEKCHRWTSCEKKGIVGHTVNTDVC 186  
 RESULT 7  
 VT2\_SFVKA STANDARD; PRT; 325 AA.  
 ID VT2\_SFVKA  
 AC P25943;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
 GN TNFRSF5 OR CD40.  
 OS Shope fibroma virus (strain Kasz). (SFV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

CC Leporipoxvirus.  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=87321103; PubMed=2820128;  
 RA Upton C., Delange A.M., McFadden G.;  
 RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the  
 RT telomeric region of the Shope fibroma virus genome";  
 RL Virology 160:20-30(1987).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=91207415; PubMed=1850261;  
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,  
 RA McFadden G., Goodwin R.G.;  
 RT "2 open reading frame from the Shope fibroma virus encodes a soluble  
 RT form of the TNF receptor";  
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).  
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL: M17433; NOT ANNOTATED\_CDS.  
 DR EMBL: A23727; CA01687.1; -;  
 DR PIR: B43692; B43692.  
 DR HSSP: P19438; 1TNR.  
 DR INTERPRO: IPR001368; -;  
 DR PRAM: PF00020; TNFR\_C6; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
 KW Receptor; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 325  
 FT DOMAIN 27 186  
 FT REPEAT 27 62  
 FT REPEAT 63 104  
 FT REPEAT 105 147  
 FT REPEAT 148 186  
 FT CARBOHYD 105 105  
 FT CARBOHYD 181 181  
 FT CARBOHYD 205 205  
 FT CARBOHYD 238 238  
 SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 22.8%; Score 226; DB 1; Length 325;  
 Best Local Similarity 30.3%; Pred. No. 8, 7e-13;  
 Matches 53; Conservative 18; Mismatches 68; Indels 36; Gaps 5;

QY 15 GHO-----LLDCKCAPGTLYLKOHCTVRRKTLVCPDPHSYTDSDWHTSDECVYCSPVCKEL 69  
 DB 30 GHDEKDGTLCCASCHPFGYASRLCGPSNTVCSPECDGTFTASTNHPACVSCGPGCTGH 89  
 QY 70 QSKVQCEKRNTHNRYCEEEERYLEIE-----FLKLRSCPPSGGVQAGTPERNYCKK 123  
 DB 90 LSSQPDNRTHRYCNCSTGYCLLKQNGCRICAPOTKCPAGYG-VSGHTRGDTLCEK 148  
 QY 124 CPDQFSGETSSKAPC-----IKHTNCSFEGLLILQKGNATHNV 163  
 DB 149 CPHHTYSLSLSPERGCTSPNTYSVGFNLXPVNDTSCIT-----TAGHNEV 194

RESULT 8  
 WT2\_MXVL  
 ID WT2\_MXVL  
 AC P29825;  
 STANDARD; PRT; 326 AA.

DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
 GN T2.  
 OS Myxoma virus (strain Lausanne).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Leporipoxvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91335768; PubMed=1651597;  
 RA Upton C., Macen J.L., Schreiber W., McFadden G.;  
 RT "Myxoma virus expresses a secreted protein with homology to the tumor  
 RT necrosis factor receptor gene family that contributes to viral  
 RT virulence";  
 RL Virology 184:370-382(1991).  
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL  
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC  
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 CC  
 CC EMBL: M95181; AAA46632.1; -;  
 DR EMBL: A23729; CA01688.1; -;  
 DR PIR: A40566; GQVZML.  
 DR HSSP: P19438; 1TNR.  
 DR INTERPRO: IPR001368; -;  
 DR PRAM: PF00020; TNFR\_C6; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 326  
 FT DOMAIN 27 186  
 FT REPEAT 27 62  
 FT REPEAT 63 104  
 FT REPEAT 105 147  
 FT REPEAT 148 186  
 FT CARBOHYD 105 105  
 FT CARBOHYD 181 181  
 FT CARBOHYD 205 205  
 FT CARBOHYD 238 238  
 SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292EF CRC64;

Query Match 21.2%; Score 211; DB 1; Length 326;  
 Best Local Similarity 29.8%; Pred. No. 1, 7e-11;  
 Matches 45; Conservative 20; Mismatches 64; Indels 22; Gaps 3;

QY 18 ILCDKCAPGTLYLKOHCTVRRKTLVCPDPHSYTDSDWHTSDECVYCSPVCKELQSVKQEN 77  
 DB 38 LCTSCPPSGYASRLCGPSDVTVCSPCKNETFTASTNHPACVSCGRCRGLHLSSEQSCD 97  
 QY 78 RTHNRYCEEEERYLEIE-----FLKLRSCPPSGGVQAGTPERNYCKKCPDGFPSG 131  
 DB 98 KTRDRAVDCSAGNYCLLKQNGCRICAPKCPAGYG-VSGHTRGDTLCTKCPRYTSD 156  
 QY 132 ETSSKAPC-----IKHTNCSF 147  
 DB 157 AVSSTETCTSSSFYISVEFNLXPVNDTSCIT 187

RESULT 9  
 VC22\_VARY  
 ID VC22\_VARY  
 AC P34015;  
 STANDARD; PRT; 349 AA.



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DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
RN
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sendakhevich L.S.;
RT *Genes of variola and vaccinia viruses necessary to overcome the host
    protective mechanisms.
    -1- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC -----
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CC -----
DR EMBL; X69198; CAA49137.1; .
DR EMBL; X67117; CAA47540.1; .
DR PIR; D36858; D36858.
DR PIR; S35987; S35987.
DR PIR; S46888; S46888.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR001368; .
DR PFAM; PF00020; TNFR_c6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Repeat.
KW DOMAIN 31 108 2 X TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; D45DA0B5C6E780EF CRC64;

Query Match. 21.2%; Score 210.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. NO. 2e-11;
Matches 48; Conservative 19; Mismatches 76; Indels 17; Gaps 4;

QY 10 YDPENG-----HQLCDKCAAGTYLKHQHTYRRKTLVCPYCPDHSYTDSDWHTSDECV 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 25 YTPPGKCKDTEYKRHNHLCCLSCPGETYASRLCDSKRTYQCPCSGGFTSRNNHLPACL 84
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 YCSPVCKELQSVKQRCNTHNHNVCCECGRYLEI-----EFCILKHSQCPGSGVYQAGT 114
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 SCNGRCNSNNOVETRNCNTNTHNRICCSFQYICLLHGSSGCKACVQSYOTKCGIGYG-VSGHT 143
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 115 PERNTVCKKCPDGFEGSETSSKAPCIKHTNCSFTGLLIQ 154
    : : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 SVGVICSPCGFGTYSHTVSSADKCEPVPN-NTFNVIDVE 182
    : : | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
ID TNRC_MOUSE STANDARD: PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTRP OR TNFCR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GN . [1]

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RP SEQUENCE FROM N.A.
RC STAIN-CVB: TISSUE=LUNG:
RX MEDLINE=96072804; PubMed=7594541.
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5280(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
sequence trap and chromosomal mapping."
RL GENOMICS 30:312-319(1995).
CC -I- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS A LA-NGER/TNR-TYPE CYSTEINE-RICH REGI
CC -----
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CC -----
DR EMBL; U29173; AAA69864.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSSP; P25942; 1CDF.
DR MCD; MG1:104875; LTBR.
DR INTERPRO: IPR001368; -
DR PFAM: PF000020; TNR_C6; 3.
DR PROSITE; PS00652; TNR_NGR_1; 2.
DR PROSITE; PS00550; TNR_NGR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMB 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 20.5%; Score 203.5; DB 1; Length 415;
Best Local Similarity 28.1%; Pred. No. 9.5e-11;
Matches 48; Conservative 26; Mismatches 84; Indels 13; Gaps 7;

OY 9 HYDETGHOLLCKACAPPTYLKOHGTIVRKTLCAVCPDHSYTDSDSWNTDECVYCSPTK 68
Db 50 YEPEA-HDVCCSRPPEEFPAVACSRSQDYVCKTCRPNSTNEHNHNLSTOGLCRP-CDI 115
OY 69 LOSVKQ--ECNRTHNRVCEBGR---YLEIE--FLKLR--SCPPGS-GVAOQSTPEVN 118

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Db 107 VLGFEEVAPCTSPKACRCOPGMSVCYLLDNECVHCEERLVLCOPSTEAETDIDMTD 166  
 QY 119 TVCKKCDGFESESSKAPCIKHTNCSFTGLILLIOGNATHDVGSGNRE 169  
 Db 167 VNCVPCKPFGHONTSPRARCOPHTRCIOGLVEADPGTSTSDTCNPPE 217

RESULT 11  
 NGFR\_HUMAN  
 ID NGFR\_HUMAN STANDARD; PRT; 427 AA.  
 AC P08138;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR) (P75 ICD).  
 GN NGFR OR TNFRSF16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87051725; PubMed=3022937;  
 RA Johnson D., Lananan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,  
 Bothwell M., Chao M.;  
 RT "Expression and structure of the human NGF receptor.";  
 RL Cell 47:545-554(1986).  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=89096903; PubMed=2850481;  
 RA Sehgal A., Palli N., Chao M.;  
 RT "A constitutive promoter directs expression of the nerve growth factor  
 receptor gene.";  
 RL Mol. Cell. Biol. 8:3160-3167(1988).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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 CC -----  
 CC EMBL: M14764; AAB59544.1; -;  
 CC EMBL: M21621; AAA36363.1; -;  
 CC PIR: A25218; GQHUN.  
 CC HSSP: P07174; INGR.  
 CC MIM: 162010; -;  
 CC INTERPRO: IPR000488; -;  
 CC INTERPRO: IPR001368; -;  
 CC PFAM: PF00020; TNFR\_c6; 4.  
 CC PFAM: PF00531; death; 1.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE: PS00650; TNFR\_NGFR\_2; 4.  
 CC PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 CC Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;  
 CC Phosphorylation; Signal.  
 CC SIGNAL 1 28  
 CC CHAIN 29 427  
 CC DOMAIN 29 250 LOW-AFFINITY NERVE GROWTH FACTOR  
 CC TRANSMEM 251 272 RECEPTOR.  
 CC DOMAIN 273 427 EXTRACELLULAR (POTENTIAL).  
 CC DOMAIN 31 189 CYTOPLASMIC (POTENTIAL).  
 CC 4 X TNFR-CYS.

FT REPEAT 31 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 147 TNFR-CYS 3.  
 FT REPEAT 148 189 TNFR-CYS 4.  
 FT DOMAIN 344 421 DEATH DOMAIN.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 89 107 BY SIMILARITY.  
 FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...)(POTENTIAL).  
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 19.48; Score 192.5; DB 1; Length 427;  
 Best Local Similarity 34.18; Pred. No. 8, 6e-10;  
 Matches 45; Conservative 21; Mismatches 55; Indels 11; Gaps 5;

QY 20 CDKCAPGTGYKOHCTVYKRTLCVPCPDH-SYTDHMTSDCEVCSPVCKELOSVKOECHN 18  
 Db 44 CKACNLGEGVAOPCGA-NQTVCEPCLDSTVFSVNAETECRCCTE-CVGLQSMAPG 101  
 QY 79 THNRVCECEGRYLE-----IEFCLKHSRCPGSGVQAGTPRNATVCKKCPDGFSGET 133  
 Db 102 ADVAVRCAGAYGQDETGTGRCEAC--RVCEAGSLGVSCQDKNTVCCECPDGTYSIM 158  
 QY 134 SSKAPCIKHTNC 145  
 Db 159 NHVDPCLPCTVC 170

RESULT 12  
 NGFR\_RAT  
 ID NGFR\_RAT STANDARD; PRT; 425 AA.  
 AC P07174;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR) (P75 ICD).  
 GN NGFR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87115859; PubMed=3027580;  
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;  
 RT "Gene transfer and molecular cloning of the rat nerve growth factor  
 receptor.";  
 RL Nature 325:593-597(1987).  
 RN [2]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE=93077038; PubMed=1446821;  
 RA Metis M., Timmusk T., Allikmets R., Saarma M., Persson H.;  
 RT "Regulatory elements and transcriptional regulation by testosterone,  
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";  
 RL Gene 121:247-254(1992).  
 RN [3]  
 RP STRUCTURE BY NMR OF 334-418.  
 RX MEDLINE=97449145; PubMed=9305641;  
 RA Liepinsh E., Ilag L.L., Orling G., Ibanez C.F.;  
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";  
 RL EMBO J. 16:4999-5005(1997).





RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD:

RX MEDLINE=94085794; PubMed=8262389;

RA Schwarz H., Tuckwell J., Lotz M.;

RT "A receptor induced by lymphocyte activation (ILA): a new member of

the human nerve-growth-factor/tumor-necrosis-factor receptor

family.";

RL Gene 134:295-298(1993).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD:

RX MEDLINE=95347766; PubMed=7622190;

RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,

Kwon B.S.;

"Characterization of human homologue of 4-1BB and its ligand.";

Immunol. Lett. 45:67-73(1995).

-I- FUNCTION: RECEPTOR FOR THE POTATIVE CYTOKINE 4-1BBL. POSSIBLY

ACTIVE DURING T CELL ACTIVATION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T

CELLS.

-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

-I- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".

-----

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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

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EMBL: U03397; AAA53133.1;

DR EMBL: L12964; AAA62478.1;

DR HSSP: P19438; TEXT.

DR MIM: 602250;

DR INTERPRO: IPR001368;

DR PFAM: PF00020; TNFR\_c6; 2.

DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE: PS00650; TNFR\_NGFR\_2; 1.

KM Receptor; Glycoprotein; Repeat; Signal; Transmembrane.

REPEAT: 1 17

SIGNAL 1 17

CHAIN 18 255

DOMAIN 18 186

TRANSMEM 187 213

DOMAIN 214 255

DOMAIN 47 159

REPEAT 47 86

REPEAT 87 118

REPEAT 119 159

CARBOHYD 138 138

CARBOHYD 149 149

CONFLICT 107 107

SEQUENCE 255 AA; 27899 MM; F3A563FE5EF00460 CRC64;

-----

Query Match 16.8%; Score 167; DB 1; Length 255;

Best Local Similarity 27.5%; Pred. No. 8.3e-08;

Matches 44; Conservative 24; Mismatches 72; Indels 20; Gaps 6;

-----

OY 8 LHYDETFGHQLCDKCAFGTYLKQHCIVTRKTLGVPCPDHSTYDS--WHTSDECVYCSPV 65

DB 16 LNFERTSLQDPDCSNCIPAGTF----CDNNRNQICSPCPNPSSTSGAGQRTCDICRCKGV 71

OY 66 KELOSVAQECNRHNRVCECEEGRYLEIFRC-LKHSRCPGSGVVGAGTPERNVTCKKC 124

DB 72 FR---TRKECSSTSNACDCTPGFHCAGAGSCMCEQDCKQGOELTKKG-----CKDC 120

OY 125 PDGFSGETSSAPCIKHTNCTFGLLLIQQGNATHDNVC 164

DB 121 CFGTFNDQ--KRGICRPWNTCSLDGKSVLVNGTKERDYYC 158

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2001, 11:23:12 ; Search time 25.38 Seconds  
(without alignments)  
462.837 Million cell updates/sec

Title: US-09-389-545-2\_COPY\_22\_194  
Perfect score: 993  
Sequence: 1 ETLPKYLHDPETGHLIC.....QKGNATHDNCNGREATOK 173

Working table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	30.2	459	2	1A8854 gene murine tumour
2	298	30.0	461	1	A35356 tumor necrosis fac
3	297	29.9	474	1	B38634 tumor necrosis fac
4	270	27.2	289	2	A46515 B cell-associated
5	270	27.2	305	2	A46476 B cell-associated
6	261	26.3	277	2	A60771 B-cell activation
7	242.5	24.4	435	2	154182 tumor necrosis fac
8	226	22.8	325	2	B43692 T2 protein - rabbi
9	211	21.2	326	1	GOVZML T2 protein - myxom
10	210.5	21.2	348	2	T28623 hypothetical prote
11	210.5	21.2	349	2	D36858 gene G4R protein -
12	209.5	21.1	349	2	D72175 G2R protein - vari
13	192.5	19.4	427	1	GOHUN nerve growth facto
14	188.5	19.0	425	1	A26431 nerve growth facto
15	184	18.5	416	1	UN0006 nerve growth facto
16	177	17.8	256	2	B32393 T-cell antigen 4-1
17	167	16.8	255	2	138426 4-1BB - human
18	166	16.7	255	2	JT0752 lymphocyte activat
19	163	16.4	271	2	S12783 OX40 antigen precu
20	160	16.1	455	1	GOHUT1 tumor necrosis fac
21	159	16.0	454	1	GOHST1 tumor necrosis fac
22	159	16.0	454	2	157826 tumor necrosis fac
23	159	16.0	461	2	JC4302 tumor necrosis fac
24	152	15.3	272	2	148700 tumor necrosis fac
25	148	14.9	461	1	GORTT1 gene ox40 protein
26	145	14.6	277	2	137552 tumor necrosis fac
27	144.5	14.6	314	2	137383 OX40 homolog - hum
28	144	14.5	335	2	A40036 Fas soluble protei
29	139	14.0	595	2	A42086 apoptosis-mediati
					CD30 antigen precu

30	137.5	13.8	324	2	JC2395 Fas antiu', precu
31	137	13.8	327	2	A46484 apoptosis radiatin
32	125	12.6	899	2	GO2428 subtilisin-like pr
33	125	12.6	915	2	JC6148 subtilisin-like pr
34	125	12.6	1680	2	A43434 furin (EC 3.4.21.7
35	120	12.1	786	2	A48456 oocyst wall protei
36	120	12.1	1252	2	S36016 oocyst wall protei
37	119.5	12.0	1548	2	S34583 serine proteinase
38	118.5	11.9	260	1	A46517 CD27 antigen precu
39	118.5	11.9	1609	1	MMHUB2 laminin gamma-1 ch
40	115.5	11.6	1111	2	T26972 hypothetical prote
41	114.5	11.5	643	2	T25473 hypothetical prote
42	113.5	11.4	1607	1	MMMSB2 laminin gamma-1 ch
43	111	11.2	1955	1	ACGH aglin precursor -
44	109.5	11.0	250	1	A49053 CD27 antigen precu
45	109.5	11.0	667	2	A48579 trophectoderm surfac

## ALIGNMENTS

RESULT 1  
1A8854 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C.Species: Mus musculus (house mouse)  
C.Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
C.Accession: 1A8854  
R.Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A.Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A.Reference number: 1A8854; MUID:95178848  
A.Accession: 1A8854  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-459 <RES>  
A.Cross-references: EMBL:X76401; NID:q43830; PIDN:CA53981.1; PID:q.4831  
A.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
F.151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 30.2%; Score 300; DB 2; Length 459;  
Best Local Similarity 35.2%; Pred. No. 1.2e-16;  
Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;  
QY 10 YPEFGH-----QLCDKCAFGTYLKQHCYTRKTLVPCPDHSYTSWHTS 56  
DB 17 YKPEGEYEQISOEYRRAKQCAKCPGQYVKKHFCNKTSPTVCADCEASWYQVWNP 76  
QY 57 DDCVYCSPYCKELOSQKOCNFRHNVCECEGRYLETF-----CLKHSCPGSGY 109  
DB 77 KCLCSGSSCSTDQYETRACTQONRVCCCEAGRCALCKTHSGSCROCKRLSKCGPG 136  
QY 110 VQAGPERNTVCKKCPDGFSEGTSSKAPCIRKHTNCSFFGLLLQKGNATHDNVCS 155  
DB 137 ASSRAPNGNVLCACAPGFSTSTSDVCBPHRCS---ILAIIPGNASTAVCA 194  
RESULT 2  
A35356 tumor necrosis factor receptor type 2 precursor - human  
N.Alternate names: 75K tumor necrosis factor receptor  
C.Species: Homo sapiens (man)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C.Accession: A35356; A36475; A48416; A36007; A23666; B35010; 138094  
R.Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990  
A.Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
A.Reference number: A35356; MUID:90260639  
A.Accession: A35356  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-461 <SMI>  
A.Cross-references: GB:M32315; NID:g189185; PIDN:AA59929.1; PID:g18:186

R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring A:Reference number: A36475; MUID:91045991

A:Accession: A36475

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195, 'R', 197-461 <KOH>

A:Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758

R:Dombo, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990

A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690

A:Accession: A48416

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 23-461 <DEM>

A:Cross-references: GB:S63368; NID:9235648; PIDN:AA19824.1; PID:9235649

A:Note: Sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)

R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration A:Reference number: A36007; MUID:90349572

A:Accession: A36007

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>

A:Cross-references: GB:M5857; NID:9339751; PIDN:AAA63262.1; PID:9339752

R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 2031-2038, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis A:Reference number: A23666; MUID:91056048

A:Accession: A23666

A>Status: preliminary

A:Molecule type: protein

A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A:Reference number: A35010; MUID:90110215

A:Accession: A35010

A>Status: preliminary

A:Molecule type: protein

A:Residues: 27-31 <EMG>

R:Kühnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994

A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934

A:Accession: I38094

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-37 <RES>

A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701

A:Status: preliminary

A:Gene: GDB:TNR2

A:Cross-references: GDB:125914; OMIM:191191

A:Map position: 1p36.2-1p36.2

A:Introns: 26/3

A:Note: the list of introns is incomplete

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-416/Product: tumor necrosis factor receptor type 2 #status experimental <MAT>

F:40-76/Domain: NGF receptor repeat homology <NG1>

F:78-119/Domain: NGF receptor repeat homology <NG3>

F:120-162/Domain: NGF receptor repeat homology <NG3>

F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>

F:280-461/Domain: intracellular #status predicted <INT>

F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

30.0%; Score 298; DB 1; Length 461;

Best Local Similarity 35.6%; Pred. No. 1.7e-16; Indels 22; 3; Matches 62; Conservative 15; Mismatches 75;

OY 10 YDPETGH-----OLCDKCAPGTLYKOHCTVRKRLTCVCPDHSYDSTMTSP 57

DB 32 YAPPGSTCRRLREYDDTADMCCKSPGQAHAFVCTKRTSDYDSCDESDSTYQJLMMV 91

OY 58 ECVYCSFVCKELOSVOECNRTNHRVCECEGRYLEI-----EFLKHSRCPGSGV 11

DB 92 ECLSGSRGSSDVOETACRQNRICRPRGWICALSKOGCRLCAPLKRKRCRGFCVAR 151

OY 112 AGPERNTVCKKCPDGFSSGTSKAPCIKHTNSTGGLILKGNATHNVCS 165

DB 152 PGETSDVCKPCAPGFSMTSTSDICRPHQICNVVAI-----PGNSMAPAVCT 201

RESULT 3

B38634

Tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 23-Jul-1999

C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tarragila, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wu, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor A:Reference number: A38634; MUID:91187885

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEM>

A:Cross-references: GB:M60469; NID:919827; PIDN:AAA39752.1; PID:919827

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors A:Reference number: A40254; MUID:91246168

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:M60469; NID:919827; PIDN:AAA39752.1; PID:919827

R:Kisonegishi, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine type 1 TNF receptor A:Reference number: S54816

A:Accession: S54816

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <KTS>

A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C:Keywords: cytokine receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F:40-77/Domain: NGF receptor repeat homology <NG1>

F:79-110/Domain: NGF receptor repeat homology <NG4>

F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 29.9%; Score 297; DB 2; Length 474; Best Local Similarity 35.2%; Pred. No. 2e-16; Matches 62; Conservative 17; Mismatches 73; Indels 24; 3;

OY 10 YDPETGH-----OLCDKCAPGTLYKOHCTVRKRLTCVCPDHSYDSTMTSP 57

DB 32 YKPEPGEGCQISDQYDRKQMCACKPPQGYVHFENKTSDFVACADCEASMTYQVNOF 91

OY 57 DECVYCSFVCKELOSVOECNRTNHRVCECEGRYLEI-----CLKHRSRCPGSGV 99

DB 92 RTCLSCSSSTTDOVEIRACTQDQNRVCAEAGRYCALKTHSGSCRCMPLSKCGPFGV 151

OY 110 VQAGTPEARNVCKKCPDGFSSGTSKAPCIKHTNSTGGLILKGNATHNVCS 166

DB 152 ASSRAPNGNVLCRACAGTFSSTTSYDVCPRHRTCS-----IIAIPGNASTAVCA 203



```

RESULT 4
A:Accession: A46515
B:cell-associated surface molecule CD40, short splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
C:Accession: A46515
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne
J. Immunol. 149, 3921-3926, 1992
A>Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:9304586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Residue type: nucleic acid
A:Residues: 1-289 <GR>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126;
experimental source: GB:BA1B/C, liver
Note: sequence extracted from NCBI backbone (NCBI:120357)
C:Comment: For an alternative splice form, see PIR:A46476
C:Superfamily: CD27 antigen; NCF receptor repeat homology
C:Keywords: alternative splicing
F:105-144/Domain: NCF receptor repeat homology <NGF>

```

```

Query March 27.2% Score 20.1; DB 2: Length 289;
Best Local Similarity 34.5%; Pred. No. 1.8e-14;
Matches 57; Conservative 26; Mismatches 66; Indels 14; Gaps 5;

QY      6 KYLHDPETGHQLLDCKDCAPIYYLKQHCTVRRRTKLCVPCPDHSYTDSWHTDEC---VYC 62
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db       30 QYLH-DGQ-----CCDLCPGSRILTSHCFTALEKTQCHPDCSGEFAQNMREIRCHQRHC 83
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

QY      63 SPVCELSVSVQEOECRNTNRNVCCEGEGRLL--ELIEFLKHNSCPRGSSVYAGRPERRT 119
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db       84 EP--NQGLRVKKEGTAESDYVTCKEGQHCSKDDEACQAQHPRCIPGFCVMEMATEETDT 141
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

QY      120 VCKKCPDGFSEFSGSTSSKAPCIKHTNCSTFGILLIIOGNATHDNVC 164
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db       142 VCHPCPVGVFFSNOSSLFKCYCWPMTSCEDKNLEVLAKGTSTQTAVIC 186
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

RESULT      5
A66476
B cell-associated surface molecule CD40, long splice form - mouse
Species: Mus musculus (house mouse)
Date: 18-Jun-1993 #sequence_1993
Accession: A66476
J.Torres, R.M.; Clark, E.A.
J.Immunol. 140, 620-626, 1992
A.Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A.Reference number: A66476; MUID:92105763
A.Accession: A66476
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-305 <TOR>
A.Cross-references: GB:M83312; NID:g1553058
A.Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
A.Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
C.Comment: For an alternative splice form, see PIR:A46515
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Keywords: alternative splicing; transmembrane protein
P:105-144/Domains: NGF receptor repeat homology <NGF>
```

```

Query Match 27.2% Score 270; DB 2; Length 305;
Best Local Similarity 34.5%; Pred. No. 1.9e-14;
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5

QY 6 KYLAHPETGHOILDKCAPGTYLKONCHTARKRTLCVPCPDHSYTDSPWTSDEC---VYC 62
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 30 GYLH-DGQ-----CCDLCQPSRLSHCTALEKTCQHPDCDSGFSAQMWREIRCHQHRNC 83
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 63 SPVCKELOSVKRCEKCNTRHVRVCECEEGGRLL---ELIFCLKHSKCPGSGSVVQAGTERTPT 119
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

D0 84 EP - N0GLRVKKEGTAE8DYCTCKEGHCHTCKDEACQHTPCIPGFGWENATE7TUT 1411

QY 120 VCKKCPDGFSEGTSSKAPCLKHTNCSFFGLLLQKGNATHDNC 164  
|| || |||| : || - : || : |||| : : ||

D0 142 VCHPCPYGFFSNQSSLFERKCPWYNSCEDKNLEVLQKGTSSQYNVIC 186

RESULT	6
A60771	

B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)

CiteDate: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-1993  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J 8 1403-1410 1989

A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608  
A:Accession: S04460

A: Molecule type: mRNA  
A: Residues: 1-277 <STA>  
A: Cross-references: EMBL:X60592; NID:q29850; PIDD:CA443045.1; PID:q29851

R. Bjaerbaek, S. Paulie, S. Koho, H. Nika, H. Aspenstroem, P. Perlmann, P. U. Immunol. 142, 562-567, 1989

Article Biochemical characteristics and partial amino acid sequence of the receptor-

A:Reference number: A60771; MUID:89093941  
A:Accession: A60771  
A:Molecule type: protein

A:Residues: 21-50 <BR>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics: none

A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
A:Genemaplink: cp33444  
A:Genemaplink: cp33444

C:superfamily C2D; antigen; ncr; lectin; repeat; homology  
C:keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; leucine-rich prot  
F:1-20/Domain: signal sequence #status predicted <Sig>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <Mat>

F:21-193/Domain:	social interaction	processes	<EXT>
F:21-193/Domain:	extracellular	#status predicted	<EXT>
F:194-215/Domain:	transmembrane	#status predicted	<ITM>
F:216-277/Domain:	intracellular	#status predicted	<CYT>

F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	26.3%	Score 261	DB 2	Length 277	✓
Best Local Similarity	33.9%	Pred. No. 9e-14			✓✓
Matches 58	Conservative 23	Mismatches 74	Indels 16	Gaps 4	✓

[illegible]

DB 18 VHPETACREKQYLLINSQCSLQCPQKVLVSDCTETETETECBPGSEBFLDWTNRRTIC //  
QY 60 ---VYCSPLCKELQSVKQECNTHNRYCECEGRVL---EIECLKHNSCPGSGVQAG 113

Db 78 H0HKYCDPMNG--LRV00KGTSETDITICTCEGWHCTSEACESECVLHRTSCSPGFGVQIA . 45

Db 136 TGVSDTICPCPCPGVGFSSVSSAFKCHPMTSCETDVLVQAGCNKTKDYVC 186

RESULT 7  
154182

tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence-revision 24-May-1996 #text-change 17-Mar-2000

C;Accession: 154182  
R;Baels, M.; Chaffenet, M.; Cassiman, J.J.; Van den Bergh, H.; Marynen, P.  
Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hmcDNA library of human 12p transcribed seq  
A:Reference number: 154182; MUID:93252381  
A:Accession: 154182

A: status: preliminary; translated from GB/EMBL/DBJ





F:67-108/Domain: NGF receptor repeat homology <NG2>  
 F:109-147/Domain: NGF receptor repeat homology <NG3>  
 F:149-189/Domain: NGF receptor repeat homology <NG3>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-427/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 192.5; DB 1; Length 427;  
 Best Local Similarity 34.1%; Pred. No. 3.2e-08;  
 Matches 45; Conservative 21; Mismatches 55; Indels 11; Gaps 5;

QY 20 CDKAPGTYLKQHCYRRKTLVPCPDH-SYDMSHTSDECVYSPVCKELQSVKQECNR 78  
 DB 44 CKACNLGEGVQPCGA-NQTVCEPLDVTFSVDVSAPEPCPKTE-CVGLHSMAPCPE 101  
 QY 79 THNRVCEBEGRYLE-IFCLKHSRCPGSGVVOAGTPERNYCKKCPDGFSGETS 133  
 DB 102 ADDAVRCRAYGYODETGHCEACSVCEGSLVFCODKONTVCEECPCGTYSDEA 158  
 QY 134 SSKAPCIKHTNC 145  
 DB 159 NHVDPCLPCTVC 170

RESULT 14  
 A:26431  
 nerve growth factor receptor precursor, low affinity - rat

N:Alternate names: NGF receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A26431; PH1229  
 R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
 Nature 325, 593-597, 1987

A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
 A:Reference number: A26431; MUID:87115859  
 A:Accession: A26431

A:Molecule type: mRNA  
 A:Residues: 1-425 <RAD>  
 A:Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756  
 R:Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.

A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid  
 A:Reference number: PH1229; MUID:93077038  
 A:Accession: PH1229

A:Molecule type: DNA  
 A:Residues: 1-20 <MEM>

A:Cross-references: GB:X61269  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w  
 C:Genetics:

Introns: 20/3

Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F:1-99/Domain: signal sequence #status predicted <SIG>  
 F:30-425/Product: nerve growth factor receptor #status predicted <MAT>  
 F:30-251/Domain: extracellular #status predicted <EXT>  
 F:33-66/Domain: NGF receptor repeat homology <NG1>  
 F:68-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-148/Domain: NGF receptor repeat homology <NG3>  
 F:150-190/Domain: NGF receptor repeat homology <NG4>  
 F:198-249/Region: serine/threonine-rich  
 F:252-273/Domain: transmembrane #status predicted <TRM>  
 F:274-425/Domain: intracellular #status predicted <INT>  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.0%; Score 188.5; DB 1; Length 425;  
 Best Local Similarity 33.3%; Pred. No. 6.7e-08;  
 Matches 43; Conservative 23; Mismatches 58; Indels 5; Gaps 4;

QY 20 CDKAPGTYLKQHCYRRKTLVPCPDH-SYDMSHTSDECVYSPVCKELQSVKQECNR 78  
 DB 45 CKACNLGEGVQPCGA-NQTVCEPLDVTFSVDVSAPEPCPKTE-CLGLHSMAPCPE 102

QY 79 THNRVCEBEGRYLE-IFCLKHSRCPGSGVVOAGTPERNYCKKCPDGFSGETS 136  
 DB 103 ADDAVRCRAYGYODETGHCEACSVCEGSLVFCODKONTVCEECPCGTYSDEANHV 162

QY 137 APCIKHTNC 145  
 DB 163 DPCLPCTVC 171

RESULT 15  
 JN0006  
 nerve growth factor receptor, low affinity precursor - chicken

N:Alternate names: NGF receptor  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JN0006; A60504  
 R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R  
 Neuron 2, 1123-1134, 1989  
 A:Title: Structure and developmental expression of the nerve growth factor receptor  
 A:Reference number: JN0006; MUID:9016579  
 A:Accession: JN0006

A:Molecule type: mRNA  
 A:Residues: 1-416 <LAR>  
 A:Experimental source: embryonic chick brain

R:Heuer, J.G.; Falemie-Mahie, S.; Wheeler, E.F.; Bothwell, M.  
 Dev. Biol. 137, 287-304, 1990

A:Title: Structure and developmental expression of the chicken NGF receptor.  
 A:Reference number: A60504; MUID:90152140  
 A:Accession: A60504

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA  
 A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <RNI>  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all  
 C:Comment: This protein is thought to form a high-affinity receptor when it associate  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-416/Product: nerve growth factor receptor #status predicted <MAT>  
 F:21-239/Domain: extracellular #status predicted <EXT>  
 F:24-57/Domain: NGF receptor repeat homology <NG1>  
 F:59-100/Domain: NGF receptor repeat homology <NG2>  
 F:101-139/Domain: NGF receptor repeat homology <NG3>  
 F:141-181/Domain: NGF receptor repeat homology <NG4>  
 F:182-237/Region: serine/threonine-rich  
 F:240-261/Domain: transmembrane #status predicted <MEM>  
 F:262-416/Domain: intracellular #status predicted <INT>  
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.5%; Score 184; DB 1; Length 416;  
 Best Local Similarity 30.9%; Pred. No. 1.5e-07;  
 Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

QY 20 CDKAPGTYLKQHCYRRKTLVPCPDH-SYDMSHTSDECVYSPVCKELQSVKQECNR 78  
 DB 36 CKACNLGEGVQPCGV-NQTVCEPLDVTFSVDVSAPEPCPKTE-CVGLHSMAPCPE 93  
 QY 79 THNRVCEBEGRYLE-IFCLKHSRCPGSGVVOAGTPERNYCKKCPDGFSGETS 135  
 DB 94 SDAVRCRAYGYODETGHCEACSVCEGSLVFCODKONTVCEECPCGTYSDEANF 152  
 QY 136 KAPCIKHTNCSTFGLLIQKGNATHDNC 164  
 DB 153 VDPCLPCTICEE-NEVMWKECTATSDAEC 180

Search completed: January 27, 2001, 11:23:14

Sat Jan 27 11:26:07 2001

Job time: 37 sec

us-09-389-545-2 copy\_22\_194.rpr

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Result No.	Score	Query Match	Length	DB	ID	Description
1	993	100.0	401	18	W38344	Mouse osteoprotegerin
2	936	94.3	401	18	W38343	Rat osteoprotegerin
3	887	89.3	197	17	R39945	Mutated OCIF, OCIF
4	887	89.3	272	17	R39944	Mutated OCIF, OCIF
5	887	89.3	321	17	R39949	Mutated OCIF, OCIF
6	887	89.3	326	17	R39940	Mutated OCIF, OCIF
7	887	89.3	327	17	R39941	Mutated OCIF, OCIF
8	887	89.3	349	20	W633928	Human FBN1A-070 protein
9	887	89.3	351	17	R39943	Mutated OCIF, OCIF
10	887	89.3	380	17	R39924	Mature osteoclast
11	887	89.3	390	17	R39357	Human osteoclast
12	887	89.3	391	19	W53236	Human OCIF genome

13	887	89.3	393	17	R99948	Mutated (L), OC1F
14	887	89.3	395	19	W57636	Modified (L), receptor
15	887	89.3	399	17	R99942	Mutated (L), OC1F
16	887	89.3	401	17	R99932	Mutated (L), OC1F
17	887	89.3	401	17	R99934	Mutated (L), OC1F
18	887	89.3	401	17	R99925	Full Length osteon
19	887	89.3	401	17	R99931	Mutated (L), OC1F
20	887	89.3	401	18	W53845	Mutated (L), OC1F
21	887	89.3	401	19	W53339	Human osteoblast
22	887	89.3	401	20	Y05742	Human osteoblast
23	887	89.3	401	20	W95030	Tumour necrosis fa
24	887	89.3	401	20	W83526	Human Fibroblast pro
25	887	89.3	401	21	Y43400	Osteoblast in pro
26	884	89.0	401	17	R99933	Mutated (L), OC1F
27	883	88.9	401	19	W57635	TRI receptor protea
28	877	88.3	401	17	R99935	Mutated (L), OC1F
29	861	86.7	187	17	R99950	Mutated (L), OC1F
30	861	86.7	187	21	Y77464	Primate protein, sea
31	688	69.3	360	17	R99936	Mutated (L), OC1F
32	654	65.9	360	17	R99938	Mutated (L), OC1F
33	650	65.5	359	17	R99939	Mutated (L), OC1F
34	642	64.7	143	17	R99946	Mutated (L), OC1F
35	617	62.1	359	17	R99937	Mutated (L), OC1F
36	596	60.0	154	17	R99929	Osteoclastogenesis
37	594.5	59.9	145	17	R99930	Osteoclastogenesis
38	443	44.6	106	17	R99947	Mutated (L), OC1F
39	420	42.3	245	20	Y28449	A human tumour nec
40	420	42.3	271	20	Y42184	Human mPLN, #1 pr
41	420	42.3	300	19	W66102	Amino acid sequenc
42	420	42.3	300	19	W63622	Human tumour necro
43	420	42.3	300	20	Y03099	Human tumour necro
44	420	42.3	300	20	Y42182	Human tumour necro
45	420	42.3	300	20	Y17479	Mammalian tumour n

RESULT	1
W8344	
ID	W8344 standard; Protein; 401 AA.
XX	
AC	W8344;
XX	
DT	20-APR-1998 (first entry)
XX	
DE	Mouse osteoprotegerin.
XX	
KM	Osteoprotegerin; antibody; diagnosis; affi-
KM	recombinant production; transgenic animal
KM	antisense oligonucleotide; probe; detect
KM	bone disease; osteoporosis; Paget's disea
KM	hyperparathyroidism; rheumatoid arthritis
KM	osteolytic metastasis; periodontal bone l
KM	osteopenia; murine.
OS	Mus sp.
XX	
FH	Key
FT	CDS
FT	
FT	Location/Qualifiers
FT	90..1295
FT	/tag= a
FT	/product= osteoprotegerin
XX	
PN	DE19654610-A1.
XX	
PD	26-JUN-1997.
XX	
PE	20-DEC-1996; 96DE-1054610.
XX	
PR	03-SEP-1996; 96US-0706945.
PR	22-DEC-1995; 95US-0577788.
XX	
PA	(AMGE-) AMGEN INC.





XX	29-AUG-1996.	
PD		
XX	20-FEB-1996:	96WO-IP00374.
PF		
XX	21-JUL-1995:	95JP-0207508.
PR	20-FEB-1995:	95JP-0054977.
PR		
XX	(SNOW )	SNOW BRAND MILK PROD CO LTD.
PA		
PI	Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;	
PI	Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;	
XX	WPI: 1996-402320/40.	
XX	N-PSDB: T33174.	
DR		
XX	DNA encoding osteoclastogenesis inhibitory factor protein - us	
PT	for bone resorption control, esp. treatment of osteoporosis	
PS		
XX	Claim 68; Page 121-122; 183pp; Japanese.	
CC	This sequence represents a mutated version of the full length	
CC	osteoclastogenesis inhibitory factor (OCIF) of the invention. Thi	
CC	sequence represents OCIF-CD2 in which amino acids 252-380 of t	
CC	mature OCIF protein are deleted. The OCIF of the invention	
CC	has a molecular weight by SDS-PAGE of 60 kD under reducing condi	
CC	and 120 kD under non-reducing conditions. The protein is adsorbed onto	
CC	cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg C.	
CC	deg C. OCIF is useful in the control of bone resorption and th	
CC	in the treatment and prevention of disorders of bone resorption,	
CC	osteoporosis.	

Query Match	89.3%	Score 887	UB 17	Length 272
Best Local Similarity	87.3%	Pred. No. 6,9e-70		
Matches 151	Conservative 7	Mismatches 15	Indels 0	Gaps 0
QY	1	ETLPKYLHYDPENGGHLLCDKCAPGTYLQKCHTRKRTLCVPCPDHSTYSDSMHTSDETV	40	
Db	22	etfppkylhydeestshqllcdkcpqgtylkgqctakwktvcapcdpdyttdswhtsde	81	
QY	61	YCSPVCKELQSVKQECNNTNHNVRVCECEGRYLEIEFCLKHRSQPGSGVQAGTPEBNTV	120	
Db	82	ycspsckelqyvkgecncnthmrvceckegryleiefclkhrcspqgfygvagqpern	141	
QY	121	CKKCPDGFSSGFTSSKAPCIKHTNCSFTGLLIQKGNATHDNVSGGNREATOK	173	
Db	142	ckrcpdgffsnetskapcrkhtncsfvgllltgqgnathdnicsgnsesitqk	194	
RESULT	5			
R99949	R99949	standard: Protein; 321 AA.		
AC	R99949;			
XX				
DT	23-APR-1997	(first entry)		
XX				
DE	Mutated OCIF, OCIF-CSph.			
XX				
KW	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone res			
XX	osteoporosis.			
OS	Synthetic.			
XX				
FT	Key	Location/Qualifiers		
FT	Peptide	1..21		
FT	Protein	/note="Signal peptide"		
FT		22..321		
FT		/note="Mature OCIF-CSph"		

[illegible]

OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Peptide 1..21  
 FT /note= "Signal peptide"  
 FT Protein 22..327  
 FT /note= "Mature OCIF-DDD2"  
 FT Misc-difference 273..274  
 FT /note= "Position of deletion, delta 253-326"  
 XX  
 PN W09626217-A1.  
 PD 29-AUG-1996.  
 XX  
 PD 20-FEB-1996; 96WO-JP00374.  
 XX  
 PR 21-JUL-1995; 95JP-0207508.  
 PR 20-FEB-1995; 95JP-0054977.  
 XX  
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;  
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;  
 DR WPI: 1996-402320/40.  
 DR N-PSDB: T33171.  
 XX  
 PT DNA encoding osteoclastogenesis inhibitory factor protein - useful  
 PT for bone resorption control, esp. treatment of osteoporosis  
 PS Claim 59; Page 115-116; 183pp; Japanese.  
 XX  
 CC This sequence represents a mutated version of the full length  
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This  
 CC sequence represents OCIF-DDD2 in which amino acids 253-326 of the  
 CC mature OCIF protein are deleted. The OCIF of the invention  
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions  
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto  
 CC cation-exchangers or heparin and its activity is lowered after 10 mins  
 CC at 70 deg C or 30 mins at 56 deg C, and is lost after 10 mins at 90  
 CC deg C. OCIF is useful in the control of bone resorption and therefore  
 CC in the treatment and prevention of disorders of bone resorption, e.g.  
 CC osteoporosis.  
 SQ Sequence 327 AA;

Query Match 89.3%; Score 887; DB 17; Length 327;  
 Best Local Similarity 87.3%; Pred. NO. 8.4e-70;  
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELPKRYLHYDEPETHQLLDCDKAGRTYKQCTVARRKTLVPCPDHSTDSMTSDSECV 60  
 ||||||| ||||||| ||||||| : ||| ||||| |||||||  
 DB 22 etfppkylhydeetshqllcdkcpptylkgqntakwktvcapcpdhytldswhtsdecl 81  
 QY 61 YCSPVCKELQSVKQECNRTNHNRCVCECEGRYLEIEFCLKHRSCTPGSGVVOAGTPEERNV 120  
 ||||||| ||||||| ||||||| : ||||||| ||||||| |||||||  
 DB 82 yspvckelqyvkgecnrtnhnvceckegryleiefclkhscppgfyvgagqperntlv 141  
 QY 121 CKKCPDGFSGTSSKAPCIKHTNCTGGLLIQKGNATHDNCVSGNREARQK 173  
 ||:||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 DB 142 ckrpdpdgsfnetsskaperkhtnctsvfgllltqkgnathdncsgnestqk 194

RESULT 8  
 ID W83928 standard; Protein: 349 AA.  
 AC W83928;  
 XX  
 DT 01-MAR-1999 (first entry)  
 XX  
 DE Human FTNMA-070 partial polypeptide.

XX  
 KM FTNMA-070; human; neurological disorder; diagnosis; therapy.  
 OS Homo sapiens.  
 PN W09848051-A2.  
 PN 29-OCT-1998.  
 PD 17-APR-1998; 98WO-US07714.  
 XX  
 PR 10-OCT-1997; 97US-0062017.  
 PR 18-APR-1997; 97US-0044746.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 PI Holtzman D, McCarthy SA;  
 DR WPI: 1999-024021/02.  
 DR N-PSDB: V69279.  
 XX  
 PT New isolated human FTNMA-070 and T85 proteins - used to develop  
 PT products for the diagnosis and therapy of disorders involving  
 PT cellular processes, e.g. neuronal development.  
 PS Disclosure: Fig 2; 127pp; English.  
 XX  
 CC This is the amino acid sequence of a partial human FTNMA-070  
 CC polypeptide, deduced from a partial cDNA (see V69279). Full-length  
 CC FTNMA-070 (see W83926) is claimed. It is a novel protein having:  
 CC homology to tumour necrosis factor receptor. FTNMA-070 nucleic  
 CC acids and polypeptides of the invention are useful as modulating  
 CC agents in regulating a variety of cellular processes. They can be  
 CC used for identifying compounds which bind to or modulate the  
 CC activity of the polypeptides (claimed). They can also be used in  
 CC screening assays, detection assays (e.g. chromosomal mapping,  
 CC tissue typing, forensic biology), predictive medicine (e.g.  
 CC diagnostic assays, prognostic assays, monitoring clinical trials,  
 CC and pharmacogenomics), and methods of treatment (e.g. therapeutic  
 CC and prophylactic) e.g. for neurological disorders.  
 SQ Sequence 349 AA;

Query Match 89.3%; Score 887; DB 20; Length 349;  
 Best Local Similarity 87.3%; Pred. NO. 9e-70;  
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELPKRYLHYDEPETHQLLDCDKAGRTYKQCTVARRKTLVPCPDHSTDSMTSDSECV 60  
 ||||||| ||||||| ||||||| : ||| ||||| |||||||  
 DB 44 etfppkylhydeetshqllcdkcpptylkgqntakwktvcapcpdhytldswhtsdecl 100  
 QY 61 YCSPVCKELQSVKQECNRTNHNRCVCECEGRYLEIEFCLKHRSCTPGSGVVOAGTPEERNV 120  
 ||||||| ||||||| ||||||| : ||||||| ||||||| |||||||  
 DB 104 yspvckelqyvkgecnrtnhnvceckegryleiefclkhscppgfyvgagqperntlv 163  
 QY 121 CKKCPDGFSGTSSKAPCIKHTNCTGGLLIQKGNATHDNCVSGNREARQK 173  
 ||:||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 DB 164 ckrpdpdgsfnetsskaperkhtnctsvfgllltqkgnathdncsgnestqk 216

RESULT 9  
 ID R99943 standard; Protein: 351 AA.  
 AC R99943;  
 XX  
 DT 23-APR-1997 (first entry)  
 XX  
 DE Mutated OCIF, OCIF-CC.  
 XX  
 KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.

XX OS Synthetic.  
 XX FT Key  
 FT Peptide  
 FT Protein  
 FT Protein  
 XX MO9626217-A1.  
 XX 29-AUG-1996.  
 XX 20-FEB-1996; 96WO-JP00374.  
 XX 21-JUL-1995; 95JP-0207508.  
 XX 20-FEB-1995; 95JP-0054977.  
 XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;  
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;  
 DR WPI: 1996-402320/40.  
 DR N-PSDB: T33173.  
 PT DNA encoding osteoclastogenesis inhibitory factor protein - useful  
 PT for bone resorption control, esp. treatment of osteoporosis  
 PS Claim 65; Page 119-121; 183pp; Japanese.  
 CC This sequence represents a mutated version of the full length  
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This  
 CC sequence represents OCIF-CC in which amino acids 331-380 of the  
 CC mature OCIF protein are deleted. The OCIF of the invention  
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions  
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto  
 CC cation-exchangers or heparin and its activity is lowered after 10 mins  
 CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90  
 CC deg.C. OCIF is useful in the control of bone resorption and therefore  
 CC in the treatment and prevention of disorders of bone resorption, e.g.  
 CC osteoporosis.  
 CC XX  
 SQ Sequence 351 AA;  
 Query Match 89.3%; Score 887; DB 17; Length 351;  
 Best Local Similarity 87.3%; Pred. No. 9, 1e-70;  
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ETLPPKYLHYDPETGHQLCDKCAPGYLKQHCYVRRKTLCPGPDHSDYSDSWHTSDECV 60  
 Db 22 etfppkyhyheeshtqldckcpqgtylkqhctakxkvtcapedhytswhtsdecl 81  
 QY 61 YCSPVCKELQSVKQECNRTNHRVCECEBGRYLETEFCLKHKRSCPPSGGVVOAGTPERNV 120  
 Db 82 ycspvckelqsvkqecnrtnhrvcecebgryletefclkhkrscppsgfgvvaqgtpernv 141  
 QY 121 CKKCPDGFSESTSKAPCIKHTNCSFGILLIOKGNATHNVCSGNREAROK 173  
 Db 142 ckrcpdgflfnetsskapcrkhtncsvfgillltqkgnathnicsgnsesclq 194  
 RESULT 10  
 R99924  
 ID R99924 standard; Protein; 380 AA.  
 XX  
 AC R99924;  
 XX  
 DT 22-APR-1997 (first entry)  
 XX  
 DE Mature osteoclastogenesis inhibitory factor.  
 XX

KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;  
 KW osteoporosis.  
 KW XX  
 OS Homo sapiens.  
 XX  
 PN MO9626217-A1.  
 XX  
 PD 29-AUG-1996.  
 XX  
 PF 20-FEB-1996; 96WO-JP00374.  
 XX  
 PR 21-JUL-1995; 95JP-0207508.  
 XX  
 PR 20-FEB-1995; 95JP-0054977.  
 XX  
 PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 XX  
 PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;  
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;  
 DR WPI: 1996-402320/40.  
 DR N-PSDB: T36685.  
 DR XX  
 PT DNA encoding osteoclastogenesis inhibitory factor protein - usef  
 PT for bone resorption control, esp. treatment of osteoporosis  
 XX  
 PS Claim 6; Page 62-64; 183pp; Japanese.  
 CC This sequence represents the mature osteoclastogenesis inhibitory  
 CC factor (OCIF) of the invention. The OCIF has a molecular weight by  
 CC SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-  
 CC reducing conditions. The protein is adsorbed onto cation-exchangers  
 CC or heparin and its activity is lowered after 10 mins at 70 deg.C or  
 CC 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is  
 CC useful in the control of bone resorption and therefore in the  
 CC treatment and prevention of disorders of bone resorption, e.g.  
 CC osteoporosis.  
 CC XX  
 SQ Sequence 380 AA;  
 Query Match 89.3%; Score 887; DB 17; Length 380;  
 Best Local Similarity 87.3%; Pred. No. 9, 1e-70;  
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ETLPPKYLHYDPETGHQLCDKCAPGYLKQHCYVRRKTLCPGPDHSDYSDSWHTSDECV 60  
 Db 1 etfppkyhyheeshtqldckcpqgtylkqhctakxkvtcapedhytswhtsdecl 81  
 QY 61 YCSPVCKELQSVKQECNRTNHRVCECEBGRYLETEFCLKHKRSCPPSGGVVOAGTPERNV 120  
 Db 61 ycspvckelqsvkqecnrtnhrvcecebgryletefclkhkrscppsgfgvvaqgtpernv 120  
 QY 121 CKKCPDGFSESTSKAPCIKHTNCSFGILLIOKGNATHNVCSGNREAROK 173  
 Db 121 ckrcpdgflfnetsskapcrkhtncsvfgillltqkgnathnicsgnsesclq 173  
 RESULT 11  
 R99357  
 ID R99357 standard; Protein; 390 AA.  
 XX  
 AC R99357;  
 XX  
 DT 05-MAY-1997 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor.  
 XX  
 KW Tumour necrosis factor; TNF; receptor; TNF-beta; ligand; tumour;  
 KW differentiation; immune response; autoimmune disease; inflammation;  
 KW septic shock; graft-versus-host; apoptosis.  
 XX  
 OS Homo sapiens.  
 XX

Query Match	Best Local Similarity	89.3%; Score 887; DB 17; Length 390;
Matches 151: Conservative	7; Mismatches 15; Indels 0; Gaps 0;	
1 ETLPRKYLHYDEPETHQLCDKCAPGTYLKQHCTVRRKTLVCPDPDHSYTDTSWHTSDECV 60		
22 eflppkyihydeetshqllcdkcpptylkgqhtakwktvcapcpdhytdswhtsdecl 81		
Qy 61 YCSPTCKELQSYKQCCNKRTHNRCVCEBGRYLEIEFCLKHSRCPSGSGYVQAGTEBRNTV 120		
Db 82 ycsptckelqsykqccnkrthnrcvceckegryleiefclkhscpspgfygvqagtebrntv 141		
Qy 121 CKKCPDGFSGSTSKAPCIKHTNCFGLLTIQGNATHDWCNSGNREATOK 173		
Db 142 ckrcpdgffsnetcskaperkhtncsvigllltkqgnathdnicsgnesctqk 194		
RESULT 12		
W53238		
ID W53238 standard; Protein; 391 AA.		
AC W53238;		
DT 15-JUL-1998 (first entry)		
DE Human OCIF genome DNA-2 protein.		
XX Human; OCIF; genome; osteoclast; antihypretic; osteoporosis;		
XX rheumatism; multiple sclerosis.		
XX Homo sapiens.		
XX W09807840-A1.		
XX		

Query Match	Best Local Similarity	89.3%	Score 887	DB 19	Length 391
Matches 151	Conservative 7	Mismatches 15	Indels 0	Gaps 0	
QY	1	ENTLPKRYLHYPERETHOHLLCDKCAAGTYLKLQHCYVRKRTLCVPCPDHSTYDSMHTSD			
DB	12	etfipkylhydeetshqllcdkcpqgtylqkntakwktvcapcdpdytidswhsdc			71
QY	61	YCSPYCKELOSQKOCNCFTHNVRCECEGRXYEIEFCUKHRSQSPGSGVVOAGPPEKNTV			120
DB	72	ycspckelqyvkqgcmtlmrvceckeqryleatclkhscppgfgvvaqgprer			131
QY	121	CKKCDGFGFSGSTSKAPCIKHTKNGSTFGLLIQKGNATHDNCVSGNEATOK			173
DB	122	ckrcpdcgfgfsmetskapcrkhtncsvfqltltqgnathdncsgnsesqk			184
RESULT	13				
ID	R99948				
AC	R99948	standard; Protein; 393 AA.			
XX					
AC	R99948				
XX					
DT	23-APR-1997	(first entry)			
XX					
DE	Mutated OCIF, OCIF-CBST.				
XX					
KW	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.				
XX					
OS	Synthetic.				
XX					
FT	Key	Location/Qualifiers			
FT	Peptide	1..21			
FT	/note= "Signal peptide"				
FT	Protein	22..393			

FT /note= "Mature OCIF-Cbst"  
 FT Misc-difference 392  
 FT /label= Gln371Leu  
 XX  
 XX MO9626217-A1.  
 XX  
 XX PD 29-AUG-1996.  
 XX  
 XX PF 20-FEB-1996: 96WO-JP00374.  
 XX  
 XX PR 21-JUL-1995: 95JP-0207508.  
 XX 20-FEB-1995: 95JP-0054977.  
 XX  
 XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 XX  
 XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;  
 XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;  
 XX  
 XX DR WPI: 1996-402320/40.  
 XX  
 XX DR N-PSDB: T33178.  
 XX  
 XX PT DNA encoding osteoclastogenesis inhibitory factor protein - useful  
 XX for bone resorption control, esp. treatment of osteoporosis  
 XX  
 XX Claim 80: Page 126-128; 183pp; Japanese.  
 XX  
 XX This sequence represents a mutated version of the full length  
 XX osteoclastogenesis inhibitory factor (OCIF) of the invention. This  
 XX sequence represents OCIF-Cbst in which Gln 371 is substituted by  
 XX Leu and amino acids 373-380 of the mature OCIF protein are deleted.  
 XX These changes are caused by the introduction of a restriction site in  
 XX the DNA encoding this protein. The OCIF of the invention has a  
 XX molecular weight by SDS-PAGE of 60 kD under reducing conditions  
 XX and 120 kD under non-reducing conditions. The protein is adsorbed onto  
 XX cation-exchangers or heparin and its activity is lowered after 10 mins  
 XX at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90  
 XX deg.C. OCIF is useful in the control of bone resorption and therefore  
 XX in the treatment and prevention of disorders of bone resorption, e.g.  
 XX osteoporosis.  
 XX  
 XX SO Sequence 393 AA:  
 XX  
 XX Query Match 89.3%; Score 887; DB 17; Length 393;  
 XX Best Local Similarity 87.3%; Pred. No. 1e-69;  
 XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
 XX  
 XX QY 1 ETLPKRLHDPETGHOILDKCAPGYTLKQCHTVRRKTLVCPDPHSYDSMHTSDECV 60  
 XX ||||||||| ||||||||| ||||||||| : ||: ||||| |||||||||  
 XX 22 etfpkylhydeetsqllcdkcpptgylkqhctakwkcvcapdpdyidswhstdecl 81  
 XX  
 XX QY 61 YCSFVCKEIQSVKQECNRTNRRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERNV 120  
 XX ||||||||| ||||||||| ||||||||| : ||||||||| |||||||||  
 XX 82 ycsfvckelqyvgqecnrthrvceckegylelefclkhrcppgfygvvgaqtpervntv 141  
 XX  
 XX QY 121 CKKCPDGFSGFSGTSSKAPCIKHTNCSFTFGLLLIQGNATHDNVCSGNREATOR 173  
 XX ||:||||||| ||||||||| ||||||||| ||||||||| |||||||||  
 XX 142 ckrcpdgffsnetsskapckrhncsvfglllctqgnathdnlcsqnsesctqk 194  
 XX  
 XX RESULT 14  
 XX ID W57636 standard; Protein: 395 AA.  
 XX  
 XX AC W57636;  
 XX  
 XX DT 27-AUG-1998 (first entry)  
 XX  
 XX DE Modified TRI receptor protein.  
 XX  
 XX KW TRI receptor; tumour necrosis factor receptor-1; TNF-alpha; TNF-beta;  
 XX inhibitor; tumour growth; tumour necrosis; microorganism infection;  
 XX cellular differentiation stimulation; ionising radiation; septic shock;  
 XX

KW anti-viral response; growth regulator; immune response; meningococemia;  
 KW autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria;  
 KW AIDS; therapy.  
 XX  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX  
 XX PN MO9812344-A1.  
 XX  
 XX PD 26-MAR-1998.  
 XX  
 XX PF 18-SEP-1996: 96WO-US15003.  
 XX  
 XX PR 18-SEP-1996: 96WO-US15003.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX PI Fleischmann RD, Greene JM, Ni J;  
 XX  
 XX XX WPI: 1998-217278/19.  
 XX  
 XX DR N-PSDB: V24487.  
 XX  
 XX PT New isolated tumour necrosis factor receptor - useful for develop  
 XX products for treating, e.g. tumours, auto-immune disease(s), graft  
 XX rejection, apoptosis or inflammation  
 XX  
 XX Claim 13: Fig 2; 111pp; English.  
 XX  
 XX This sequence is a tumour necrosis factor receptor-1 (TRI) recei  
 XX of the invention. The DNA can be used to produce a recombinant hu  
 XX cell by inserting it into a vector, which is then used to transfect the  
 XX host cell. The TRI receptor can bind both TNF-alpha and TNF-beta. TRI  
 XX receptor agonists can be used for inhibition of tumour growth an  
 XX necrosis of tumours. They can also be used to stimulate cellular  
 XX differentiation, e.g. T cell, fibroblasts or haematopoietic cell  
 XX against microorganisms and prevent related disease. The agonists may  
 XX also be used to protect against the deleterious effects of ionising  
 XX radiation produced during a course of radiotherapy, e.g. denatur  
 XX enzymes, lipid peroxidation or DNA damage. The agonists may further be  
 XX used to mediate an anti-viral response. The agonists may further be  
 XX the immune response and to treat immunodeficiencies related to diseases  
 XX such as HIV. Antagonists to the TRI receptor may be used to treat  
 XX autoimmune diseases, e.g. graft versus host rejection and allograft  
 XX rejection, and T cell mediated autoimmune diseases. They may also be used  
 XX to prevent apoptosis. They may also be used to prevent cytotoxicity and  
 XX to treat septic shock, meningococemia, inflammation, bacterial  
 XX infections, cachexia, cerebral malaria or AIDS. The products can also be  
 XX used for diagnosing the above diseases.  
 XX  
 XX SO Sequence 395 AA:  
 XX  
 XX Query Match 89.3%; Score 887; DB 19; Length 395;  
 XX Best Local Similarity 87.3%; Pred. No. 1e-69;  
 XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
 XX  
 XX QY 1 ETLPKRLHDPETGHOILDKCAPGYTLKQCHTVRRKTLVCPDPHSYDSMHTSDECV 60  
 XX ||||||||| ||||||||| ||||||||| : ||: ||||| |||||||||  
 XX 22 etfpkylhydeetsqllcdkcpptgylkqhctakwkcvcapdpdyidswhstdecl 81  
 XX  
 XX QY 61 YCSFVCKEIQSVKQECNRTNRRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERNV 120  
 XX ||||||||| ||||||||| ||||||||| : ||||||||| |||||||||  
 XX 82 ycsfvckelqyvgqecnrthrvceckegylelefclkhrcppgfygvvgaqtpervntv 141  
 XX  
 XX QY 121 CKKCPDGFSGFSGTSSKAPCIKHTNCSFTFGLLLIQGNATHDNVCSGNREATOR 173  
 XX ||:||||||| ||||||||| ||||||||| ||||||||| |||||||||  
 XX 142 ckrcpdgffsnetsskapckrhncsvfglllctqgnathdnlcsqnsesctqk 194  
 XX  
 XX RESULT 15  
 XX ID R99942 standard; Protein: 399 AA.  
 XX



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:38 ; Search time 41.41 Seconds

(without alignments)  
611.372 Million cell updates/sec

Title: US-09-389-545-2\_COPY\_186\_401

Perfect score: 1113

Sequence: 1 SGNREATQKCIDVTLCEEA.....QKLFLEMIGNOVQSVKISCL 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP mammal:\*  
6: SP invertebrate:\*  
7: SP\_mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	401	11	008712
2	1069	96.0	401	11	008727
3	969	87.1	401	4	000300
4	938	84.3	372	4	090HP4
5	105	9.4	636	4	09NNX2
6	105	9.4	674	4	09P010
7	105	9.4	691	4	09POX5
8	105	9.4	694	4	09UKA1
9	103	9.3	731	4	095287
10	100	9.0	535	4	090UC8
11	96.5	8.7	690	4	090UT7
12	95	8.5	203	10	040UT67
13	95	8.5	486	5	019863
14	94	8.4	729	11	088317
15	94	8.4	729	11	090YE6
16	91.5	8.2	901	11	096ZJ4
17	91	8.2	1364	13	09YHY6
18	90.5	8.1	833	5	017102
19	90	8.1	1103	4	09NNY6

20	89.5	8.0	1232	4	09NY24	09ny24
21	89	8.0	888	5	09VDD8	09vdd8
22	88.5	8.0	184	10	09L198	09l198
23	88.5	8.0	469	5	09NSN7	09nsn7
24	88.5	8.0	585	4	090007	090007
25	88.5	8.0	710	5	09XTS0	09xts0
26	88.5	8.0	1388	13	091785	091785
27	88	7.9	361	13	090608	090608
28	88	7.9	523	5	018378	018378
29	88	7.9	1225	13	090640	090640
30	88	7.9	5293	5	09V6V2	09v6v2
31	88	7.9	5385	5	09V6V3	09v6v3
32	87	7.8	823	2	067119	067119
33	87	7.8	1215	2	092771	092771
34	87	7.8	1215	2	09J5S9	09j5s9
35	87	7.8	4151	5	096936	096936
36	87	7.8	5201	5	090479	090479
37	86.5	7.8	1828	11	090YF3	090yf3
38	86	7.7	706	2	09RP72	09rp72
39	86	7.7	1442	2	09POB4	09pob4
40	86	7.7	1837	3	074424	074424
41	86	7.7	2871	4	014189	014189
42	86	7.7	2871	4	075993	075993
43	85.5	7.7	1360	13	09YGS5	09ygs5
44	85	7.6	732	5	024557	024557
45	85	7.6	732	5	024558	024558

## ALIGNMENTS

RESULT 1  
ID 008712 PRELIMINARY; PRT: 401 AA.  
AC 008712; 070202;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE OSTEOCALCIN PRECURSOR (OSTEOCALCINOGENESIS INHIBITORY FACTOR (OCIF)).  
GN INFRSFILB OR OPG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei.  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RA [1]  
RA SEQUENCE FROM N.A.  
RA STRAIN=BALB/C; TISSUE=KIDNEY;  
RA MEDLINE=97262071; PubMed=9108485;  
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shinar D., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hall D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;  
RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";  
RA Cell 89:309-319(1997).  
RL [2]  
RL SEQUENCE FROM N.A.  
RL STRAIN=129/OLA, AND NIH SWISS;  
RL MEDLINE=98382527; PubMed=9714833;  
RL MEDLINE=98382527; PubMed=9714833;  
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morita H.;  
RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";  
RL Gene 215:339-343(1998).  
CC -!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
CC -!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,  
 CC BRAIN, HEART, KIDNEY, STOMACH, SKIN, CALVARIA AND  
 CC PLACENTA. NOT DETECTED IN SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT  
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY  
 CC 15 TO DAY 17.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: U94331; AAB53708.1; -.  
 DR EMBL: AB013898; BAA28269.1; -.  
 DR EMBL: AB013903; BAA33388.1; -.  
 DR EMBL: AB013899; BAA33388.1; JOINED.  
 DR EMBL: AB013900; BAA33388.1; JOINED.  
 DR EMBL: AB013901; BAA33388.1; JOINED.  
 DR EMBL: AB013902; BAA33388.1; JOINED.  
 DR HSSP: P25942; ICDF.  
 DR MGD: MGI:109587; Opg.  
 DR INTERPRO: IPR000488; -.  
 DR INTERPRO: IPR001368; -.  
 DR PIRAM: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT DOMAIN 23 201  
 FT REPEAT 23 201  
 FT REPEAT 64 106  
 FT REPEAT 107 143  
 FT REPEAT 144 201  
 FT REPEAT 306 365  
 FT DISULFID 41 54  
 FT DISULFID 44 62  
 FT DISULFID 65 80  
 FT DISULFID 83 97  
 FT DISULFID 87 105  
 FT DISULFID 118 142  
 FT DISULFID 145 160  
 FT CARBOHYD 98 165  
 FT CARBOHYD 165 165  
 FT CARBOHYD 178 289  
 FT CARBOHYD 289 289  
 FT VARIANT 138 138  
 FT VARIANT 161 161  
 FT VARIANT 165 165  
 FT VARIANT 288 288  
 FT VARIANT 296 296  
 FT SEQUENCE 401 AA; 45923 MW; CAA6102B3B312470 CRC64;

Query Match 100.0%; Score 1113; DB 11; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2e-80;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RKTMRFLHSTMYRYLYOKLEFLEMIGNOVSVKISCL 216  
 DB 366 RKTMRFLHSTMYRYLYOKLEFLEMIGNOVSVKISCL 401  
 RESULT 2  
 ID 008727 PRELIMINARY; PRT; 401 AA.  
 AC 008727;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE OSTEOBLAST PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR  
 DE (OCIF)).  
 GN TNFRSF11B OR OPG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 OX NCBI\_Taxid=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESTINE;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luechly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimada  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patt  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT \*Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.;  
 RL Cell 89:309-319(1997).  
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: U94330; AAB53707.1; -.  
 DR HSSP: P25942; ICDF.  
 DR INTERPRO: IPR001368; -.  
 DR PIRAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; -; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT DOMAIN 23 201  
 FT REPEAT 23 201  
 FT REPEAT 64 106  
 FT REPEAT 107 143  
 FT REPEAT 144 201  
 FT REPEAT 306 365  
 FT DISULFID 41 54  
 FT DISULFID 44 62  
 FT DISULFID 65 80  
 FT DISULFID 83 97  
 FT DISULFID 87 105  
 FT DISULFID 118 142  
 FT DISULFID 145 160  
 FT CARBOHYD 98 165  
 FT CARBOHYD 165 165  
 FT CARBOHYD 178 289  
 FT CARBOHYD 289 289  
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;

Query Match 96.0%; Score 1069; DB 11; Length 401;  
 Best Local Similarity 95.4%; Pred. No. 5.9e-77;

Matches 206; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SGNREATORCGIDVTLCEAFRRFAVPTKIIPWLSVLDNLPCTKVNASVERIKRRH 60  
 DB 186 SGNREATORCGIDVTLCEAFRRFAVPTKIIPWLSVLDNLPCTKVNASVERIKRRH 245  
 QY 61 SOBQOTQOLKMKHONRQDMVKKIIODIDLCSSVORHGHNSLTTEOLLAMESLPK 120  
 DB 246 SOBQOTQOLKMKHONRQDMVKKIIODIDLCSSVORHGHNSLTTEOLLAMESLPK 305  
 QY 121 KISPEEIERTRKTKSSQOLKLLSLMRKNGDPTLKGMLYALKHLKTSHPKTYTHSL 180  
 DB 306 KISPEEIERTRKTKSSQOLKLLSLMRKNGDPTLKGMLYALKHLKTSHPKTYTHSL 365  
 DB 181 KRTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 216  
 366 KRTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401

RESULT 3  
 ID 000300 PRELIMINARY; PRT; 401 AA.  
 AC 000300; 060236;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)  
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).  
 GN TNFRSF11B OR OPG OR OCIF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 Ruehle R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,  
 Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 Davy E., Bucay N., Renshaw-Geeg L., Hughes T.M., Hill D., Pattison W.,  
 Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 Suggs S., Boyle W.J.;  
 RA \*osteoprotegerin: a novel secreted protein involved in the regulation  
 of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG FIBROBLAST;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 Tsuda E., Morinaga T., Higashio K.;  
 RA \*Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 osteoclastogenesis in vitro.";  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 RA \*Cloning and characterization of the gene encoding human  
 osteoprotegerin/osteoclastogenesis-inhibitory factor.";  
 RL Eur. J. Biochem. 254:685-691(1998).  
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES  
 OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY  
 SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO  
 OSTROCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN  
 STROMAL CELLS AND OSTEOCLAST PROGENITORS.  
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY  
 SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, H.  
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN  
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.  
 CC -1- SIMILARITY: CONTAINS A LA-NGF/TNFR-TYPE CYSTEINE-RICH RECI-  
 DR EMBL: AB002146; BAA25910.1;  
 DR EMBL: AB008822; BAA32076.1;  
 DR EMBL: AB008821; BAA32076.1; JOINED.  
 DR EMBL: U94332; AAB53709.1;  
 DR HSP; P25942; ICDF.  
 DR MIM: 602643;  
 DR INTERPRO: IPR001368;  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE: PS00505; TNFR\_NGFR\_2; 2.  
 DR PRODOM: PD000771; 1.  
 KW Glycoprotein; Repeat; Cytokine; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 401 OSTEOPROTEGERIN.  
 FT DOMAIN 23 183 4 X TNFR-CYS.  
 FT REPEAT 23 183 TNFR-CYS 1.  
 FT REPEAT 64 106 TNFR-CYS 2.  
 FT REPEAT 107 143 TNFR-CYS 3.  
 FT REPEAT 144 201 TNFR-CYS 4.  
 FT DOMAIN 306 365 DEATH DOMAIN.  
 FT DISULFID 41 54 BY SIMILARITY.  
 FT DISULFID 44 62 BY SIMILARITY.  
 FT DISULFID 65 80 BY SIMILARITY.  
 FT DISULFID 83 97 BY SIMILARITY.  
 FT DISULFID 87 105 BY SIMILARITY.  
 FT DISULFID 118 142 BY SIMILARITY.  
 FT DISULFID 145 160 BY SIMILARITY.  
 FT CARBOHYD 98 98 POTENTIAL.  
 FT CARBOHYD 152 152 POTENTIAL.  
 FT CARBOHYD 165 165 POTENTIAL.  
 FT CARBOHYD 178 178 POTENTIAL.  
 FT CARBOHYD 289 289 POTENTIAL.  
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).  
 SQ SEQUENCE 401 AA; 45996 MW; EB42FASIC9D7C7IE CRC64;

Query Match 87.1%; Score 969; DB 4; Length 401;  
 Best Local Similarity 84.7%; Pred. No. 4.7e-69;  
 Matches 183; Conservative 19; Mismatches 14; Indels 0;

QY 1 SGNREATORCGIDVTLCEAFRRFAVPTKIIPWLSVLDNLPCTKVNASVERIKRRH 60  
 DB 186 SGNREATORCGIDVTLCEAFRRFAVPTKIIPWLSVLDNLPCTKVNASVERIKRRH 245  
 QY 61 SOBQOTQOLKMKHONRQDMVKKIIODIDLCSSVORHGHNSLTTEOLLAMESLPK 120  
 DB 246 SOBQOTQOLKMKHONRQDMVKKIIODIDLCSSVORHGHNSLTTEOLLAMESLPK 305  
 QY 121 KISPEEIERTRKTKSSQOLKLLSLMRKNGDPTLKGMLYALKHLKTSHPKTYTHSL 180  
 DB 306 KISPEEIERTRKTKSSQOLKLLSLMRKNGDPTLKGMLYALKHLKTSHPKTYTHSL 365  
 QY 181 KRTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 216  
 DB 366 KRTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401

RESULT 4  
 ID 090HP4 PRELIMINARY; PRT; 372 AA.  
 AC 090HP4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE OSTROPROTEGERIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;  
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens";  
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).  
DR EMBL: AF134187; AAF20168.1; -  
DR HSSP: P25942; 1CDE.  
DR INTERPRO: IPR001368; -  
DR PFAM: PF000020; TNFR\_C6; 3.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
FT NON\_TER 1  
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CD3 CRC64;  
  
Query Match 84.3%; Score 938; DB 4; Length 372;  
Best Local Similarity 84.6%; Pred. No. 1,2e-66;  
Matches 176; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
  
OY 1 SGNRATGCGIDVTLCGEAFRFAVPKTIIPNMTSVLDSPGKVAESVERIKRRHS 60  
DB 165 SGNSESTGCGIDVTLCGEAFRFAVPKTIIPNMTSVLDSPGKVAESVERIKRRHS 224  
61 SEQQTFLKLKMKHONRDQEMVKIITDIDLCSSVQRHLSNLTQTLALMESLPK 120  
DB 225 SEQQTFLKLKMKHONRDQEMVKIITDIDLCSSVQRHLSNLTQTLALMESLPK 284  
OY 121 KISPEIERTKTKSSSEQLKLKSLMRKNGDDOTLKGMLAKHLKTSHPKTVTSHL 180  
DB 285 KVGADIDKTKTKACRPSQIILKLSLMRIKNGDDOTLKGMLAKHLKTSHPKTVTSHL 344  
OY 181 RTMRFLSFTMYRLYOKLFLEMIGNOV 208  
DB 345 KKTIRFLHSFTMYRLYOKLFLEMIGNOV 372  
  
RESULT 5  
O9NKN2 PRELIMINARY; PRT; 636 AA.  
AC O9NKN2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE CDNA FLJ20146 FIS. CLONE COL07877.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Kawabata A., Hiki J., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
Okutani R., Ota T., Suzuki Y., Oiyashi M., Nishi T., Shibahara T.,  
Tanaka T., Nakamura Y., Isonaga T., Sugano S.;  
RT "NEDO human cDNA sequencing project";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK000153; BAA90978.1; -  
SQ SEQUENCE 636 AA; 72098 MW; B541A0CD9E8DFBAF CRC64;  
  
Query Match 9.4%; Score 105; DB 4; Length 636;  
Best Local Similarity 26.3%; Pred. No. 1.6;  
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;  
  
OY 50 ESVERIKRR---HSSQDTFLK---LMKHONRDQEMVKIITDIDLCSSVQRH-IG 101  
DB 90 EELDKIKKVIAGHSCQDFTALLGLSLMWAERQKFFKYSVDEKDKAEVSEHSTG 149  
OY 102 HSNLTQTLALMESLPKTKISPEIERTKTKSSSEQLKLKSLMRKNGDDOTLKGML 161  
DB 150 ITHLPPEVMTLSIFSYL-----NPQELCRCSQVSMKWSQTLTGTSLM----- 190

OY 162 YALKHKTSHPK 174  
DB 191 ---KHLVPVHWAR 200  
  
RESULT 6  
O9P010 PRELIMINARY; PRT; 674 AA.  
AC O9P010;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE P45KRP2-LIKE PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Jin Y., Jiang C., Li  
Han Z., Wang Y., Chen Z., Fu G.;  
RT "A novel gene expressed in the human adrenal gland";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RA Ren S., Shi J., Huang C., Jiang C., Li Y., Zhou J., Yu Y., Xu  
Wang Y., Fu G., Chen Z., Han Z.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157323; AAF67489.1; -  
SQ SEQUENCE 674 AA; 76543 MW; 7B75B339DE70E7FC CRC64;  
  
Query Match 9.4%; Score 105; DB 4; Length 674;  
Best Local Similarity 26.3%; Pred. No. 1.7;  
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;  
  
OY 50 ESVERIKRR---HSSQDTFLK---LMKHONRDQEMVKIITDIDLCSSVQRH-IG 101  
DB 128 EELDKIKKVIAGHSCQDFTALLGLSLMWAERQKFFKYSVDEKDKAEVSEHSTG 149  
OY 102 HSNLTQTLALMESLPKTKISPEIERTKTKSSSEQLKLKSLMRKNGDDOTLKGML 161  
DB 188 ITHLPPEVMTLSIFSYL-----NPQELCRCSQVSMKWSQTLTGTSLM----- 228  
OY 162 YALKHKTSHPK 174  
DB 229 ---KHLVPVHWAR 238  
  
RESULT 7  
O9P0X5 PRELIMINARY; PRT; 691 AA.  
AC O9P0X5;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE F-BOX PROTEIN FLR1.  
GN FLR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Shibahara N.;  
RT "cDNA cloning of a new human protein, FLR1, containing both mol  
F-box and leucine-rich repeat";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF142481; AAF66616.1; -  
SQ SEQUENCE 691 AA; 78554 MW; 923A1B31590E5145 CRC64;

Query Match 9.4%; Score 105; DB 4; Length 691;  
Best Local Similarity 26.3%; Pred. No. 1.7;  
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSOEFOFLK--LMKHQNRDQEWKTIIDIDLCSSVORH-LG 101  
DB 145 EEKLDIKKKYIAOHCOSKDTAELRLGSLMNHAEEROKFKYSDKSEAEVSEHSTG 204  
OY 102 HSNLTTEQLALMESLPGRKISPEEIERTRKTKSSPOLKLLSLMRKNGDODTLKGLM 161  
DB 205 ITHLPPEVMSIFSYL-----NPQELCRSCQSVSMKMSQLTKTGSIM----- 245  
OY 162 YALKHLKTSHPK 174  
DB 246 ---KHLVPVHMAR 255

## RESULT 8

ID 09UKA1 PRELIMINARY; PRT; 694 AA.  
AC 09UKA1;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
DE F-BOX PROTEIN FBL5 (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Winston J.T., Elledge S.J., Harper W.;  
RT "A family of mammalian F-box proteins."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF176700; AAF03700.1;  
DR INTERPRO: IPR001611;  
DR INTERPRO: IPR001810;  
DR PFAM: PF00560; LRR; 1.  
DR PFAM: PF00646; F-box; 1.  
FT NON\_TER 1  
SQ SEQUENCE 694 AA; 78795 MW; 198D1FE13F95BC68 CRC64;

Query Match 9.4%; Score 105; DB 4; Length 694;  
Best Local Similarity 26.3%; Pred. No. 1.7;  
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSOEFOFLK--LMKHQNRDQEWKTIIDIDLCSSVORH-LG 101  
DB 148 EEKLDIKKKYIAOHCOSKDTAELRLGSLMNHAEEROKFKYSDKSEAEVSEHSTG 207  
OY 102 HSNLTTEQLALMESLPGRKISPEEIERTRKTKSSPOLKLLSLMRKNGDODTLKGLM 161  
DB 208 ITHLPPEVMSIFSYL-----NPQELCRSCQSVSMKMSQLTKTGSIM----- 248  
OY 162 YALKHLKTSHPK 174  
DB 249 ---KHLVPVHMAR 255

## RESULT 9

ID 095287 PRELIMINARY; PRT; 731 AA.  
AC 095287;  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)  
DE GOLGIN-84.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RX MEDLINE=99-15642; PubMed=9915833;  
RA Bascom R.A., Srinivasan S., Nussbaum R.L.;  
RT "Identification and characterization of golgin-84, a novel Golgi  
integral membrane protein with a cytoplasmic coiled-coil domain."  
J. Biol. Chem. 274:2953-2962(1999).  
DR EMBL; AF085199; AAD09753.1;  
SQ SEQUENCE 731 AA; 82990 MW; E708D023C60B02BA CRC64;

Query Match 9.3%; Score 103; DB 4; Length 731;  
Best Local Similarity 23.5%; Pred. No. 2.6;  
Matches 39; Conservative 36; Mismatches 75; Indels 16; Gaps 5;

OY 49 AESVERIKRRHSSOEFOFLKLMK--HQRDQEWKTIIDIDLCSSVORHLSGN 106  
DB 463 ASMELEELRHEKQREELQKLMGQIHQLRSE-----LQDME-----AQGVNAESA 510  
OY 107 TEQLALMESLPGRKISPEEIERTRKTKSSPOLKLLSLMRKNGDODTLKGLMALK 161  
DB 511 REQLDLDHQAQKASQKQLELELEKQEFHYIE-EDLYRTKNTLOSRIKRDDEI 569  
OY 167 LKTSHPKTYTHSLRKTW-RFLHSFTMYRLYOKLFLFMGNQVQSV 211  
DB 570 LRNQLTKTLSSQSELENRLHQLTETTLQKOTMLESSTENSL 615

## RESULT 10

ID 09UKC8 PRELIMINARY; PRT; 535 AA.  
AC 09UKC8;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
DE F-BOX PROTEIN FBL5 (FRAGMENT).  
GN FBL5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cenciarelli C., Chaiur D.S., Guardavaccaro D., Parks W., Vidal M.  
RA Pagano M.;  
RT "Identification of a family of human F-box proteins."  
RL Curr. Biol. 9:1177-1179(1999).  
DR EMBL; AF174591; AAF04512.1;  
DR INTERPRO: IPR001611;  
DR INTERPRO: IPR001810;  
DR PFAM: PF00560; LRR; 1.  
DR PFAM: PF00646; F-box; 1.  
FT NON\_TER 1  
SQ SEQUENCE 535 AA; 59824 MW; 110B59DF98C3F1EE CRC64;

Query Match 9.0%; Score 100; DB 4; Length 535;  
Best Local Similarity 26.4%; Pred. No. 3.2;  
Matches 32; Conservative 19; Mismatches 44; Indels 26; Gaps 4;

OY 58 RHSSOEFTPOLK--LMKHQNRDQEWKTIIDIDLCSSVORH-LGHSNLTTEQL 113  
DB 1 OHOSQKTAELRLGSLMNHAEEROKFKYSDKSEAEVSEHSTGTHLPPEVMSIF 60  
OY 114 MESLPGRKISPEEIERTRKTKSSPOLKLLSLMRKNGDODTLKGLMALKLTSHPK 173  
DB 61 FSYL-----NPQELCRSCQSVSMKMSQLTKTGSIM-----KHLVPVHMAR 198  
OY 174 K 174  
DB 99 R 99

[illegible]

RESULT	13			
019863				
ID	019863	PRELIMINARY;	PRM;	486 AA.
AC	019863;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)		
DT	01-JAN-1999	(TREMBLrel. 09, last annotation update)		
DE	F28C6.1 PROTEIN.			
GN	F28C6.1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;			
OC	Rhabditidae; Peloderiinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Burton J.;			

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RP      SEQUENCE FROM N.A.
RX      MEDLINE=94150718; PubMed=7906398;
RA      Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson
RA      Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA      Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA      Lighthill J., Lloyd C., McMurray A., Mortimore B., O'Callaghan P.,
RA      Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showkeen, R.,
RA      Smadon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA      Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA      Watson A., Weinstock L., Wilkinson-Sproat J., Woulfdan P.,
RT      "2.2 Mb of contiguous nucleotide sequence from chromosome III of
RT      elegans."
DR      Nature 368:32-38(1994).
RL      EMBL; Z68315; CAA92669.1; -
SQ      SEQUENCE 486 AA; 53618 MW; 759CF127A26BEA61 CRC64;

Query Match      8.5%; Score 95; DB 5; Length 486;
Best Local Similarity 25.1%; Pred. NO. 7.1;
Matches 56; Conservative 36; Mismatches 69; Indels 62; gaps 13.

QY      21 FFFFAVPKRIIPNMLSVYDS-IP--GTRVAAE-SVERIKR-----HSSQEQTFOLLAKT 71
      | | | | | : : | | | | | : : : : | | | : : |
DB      217 FPFTEGVPPVSSGNGVAAEYVDGRLPAVGVTRSKYDILTYDELRRRCGAPPEHNNOSALYCFEFK 476

Y      72 WKHQ---NRDQENVKIIIDIDLCSSVQRH---LGHSNLTTEQLALM-----HSA 17

```

Db 277 SKKKEAIRN-----VKKVLFDYNTVTRMQRKRVCTSPLEEDANALARDLDSITEEFL 332

QY 118 PGKKISPEELER-----TRKTKCSSEDLKLKLSMRK-NGDDOTLKG--- 159

Db 333 PIDALILEMLEKLFIPNNKNDICLRILKNTKRTTRIKTLEVRKOPRITGQKEKLGNSL 392

QY 160 -LWYALKHLKTSHF--PKYVTHSLRKTRMRFLHSFTMYRLYOKL 109

Db 393 DLSTYHNFSLTTHGFGHPNSLSH-----YRSTOKI 421

## RESULT 14

088317 PRELIMINARY; PRT; 729 AA.

Db 088317; 01-NOV-1998 (TREMBLrel. 08, Created)

Dt 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

Dt 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE RET-II PROTEIN.

GN GOLGA5 OR RET-II.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=WHOLE BRAIN;

RA Snider J., Sano H., Ohta M.;

RT "Unknown, 5' similar to RET-II mRNA."

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB016784; BAA33010.1; -

DR MGD; MGI:1351475; Golga5.

SQ SEQUENCE 729 AA; 82367 MW; 8418BEBE6E4865E1 CRC64;

Query Match 8.4%; Score 94; DB 11; Length 729;

Best Local Similarity 22.3%; Pred. No. 14;

Matches 37; Conservative 37; Mismatches 76; Indels 16; Gaps 5;

QY 49 AESVERIKRRHSQEQTFQOLKIM--KHONRODEMVKKIIDIDLCSSVQRHLGSHNL 106

Db 461 ASSMELELRHEKEMQKEIOLKMGOMHOLRSE-----LQDME-----AQQVSEASA 508

Db 107 TEQLLALMESLPKGISPEIERTRKTKSSBOLLKLSLMRIKNGDDOTLKGIMAYALKH 166

Db 509 REQLDPLDQOIAKQRTSKQELTELERMKOEFRYME-EDLHRTKNTLQSRIRKDREREIQK 567

QY 167 LKTSHPKTVTHSLRKTRMR-LHSFTMYRLYOKLFLEMIGNOVSY 211

Db 568 LRNQLNKTLSNSSQSELSRLHQLTFELIQLKQTMLESISTEKNSL 613

## RESULT 15

090Y6 PRELIMINARY; PRT; 729 AA.

Ac 090Y6; 01-MAY-2000 (TREMBLrel. 13, Created)

Dt 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

Dt 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE SUMIKO.

GN SUMIKO.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Ku P.T., You M.J., Cottam M.K., Bose H.R. Jr.;

RT "Suppression of Anti-Immunoglobulin-Induced Apoptosis in B Lymphoma Cells by a Novel Nuclear Protein."

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF026274; AAF21628.1; -

SQ SEQUENCE 729 AA; 82450 MW; 6E3389FA82361AFA CRC64;

Query Match 8.4%; Score 94; DB 11; Length 729;

Best Local Similarity 22.3%; Pred. No. 14;

Matches 37; Conservative 37; Mismatches 76; Indels 16; Gaps 5;

QY 49 AESVERIKRRHSQEQTFQOLKIM--KHONRODEMVKKIIDIDLCSSVQRHLGSHNL 106

Db 461 ASSMELELRHEKEMQKEIOLKMGOMHOLRSE-----LQDME-----AQQVSEASA 508

Db 107 TEQLLALMESLPKGISPEIERTRKTKSSBOLLKLSLMRIKNGDDOTLKGIMAYALKH 166

Db 509 REQLDPLDQOIAKQRTSKQELTELERMKOEFRYME-EDLHRTKNTLQSRIRKDREREIQK 567

QY 167 LKTSHPKTVTHSLRKTRMR-LHSFTMYRLYOKLFLEMIGNOVSY 211

Db 568 LRNQLNKTLSNSSQSELSRLHQLTFELIQLKQTMLESISTEKNSL 613

Search completed: January 27, 2001, 11:24:32

Job time: 114 sec

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CC EMBL: AJ223984: CAAL1758.1: -  
 DR EMBL: 254140: CA90815.1: -  
 KM Transmembrane; Meiosis.  
 FT TRANSMEM 285 305 POTENTIAL.  
 FT TRANSMEM 392 412 POTENTIAL.  
 FT TRANSMEM 504 524 POTENTIAL.  
 FT TRANSMEM 564 584 POTENTIAL.  
 FT TRANSMEM 926 946 POTENTIAL.  
 FT TRANSMEM 964 1004 POTENTIAL.  
 SQ SEQUENCE 1309 AA; 147412 MW; 33EEA6794DBC6A82 CRC64;

Query Match 8.3%; Score 92; DB 1; Length 1309;  
 Best Local Similarity 24.5%; Pred. No. 9.5;  
 Matches 57; Conservative 31; Mismatches 77; Indels 68; Gaps 11;

QY 1 SGNREATORCGIDVTLCEFAFFRAVPTKIIPMLSVLVSLP-----G 44  
 DB 591 SASRKATYLLGEVLRISDE-----LPIHLGAKIQSLPSLFNMAQFTAEFRVA 640  
 QY 45 TKV--NAESVERIKRRHSQ--EQTFOLKLMKHQ-----NRDOENVK-KTIODID- 90  
 DB 641 TSVLOSIESLNRKFSATQPSQTSLSL--LFKEQKTDGSEFRGQROVEHVKLMGQIJD 698  
 QY 91 -----LCSSVQRHGHGSLTTEOLLALMESLPKKISPEEIERKTKCKSSQEL--- 141  
 DB 699 SHFRSLAETNVLATKNYQKRWDTLVQIME--GPLLSPKRIDETLRTTKERRLLAFY 755  
 QY 142 -----KLISLWRIKNGDQ-----DTLKGIMVALKHLKTSHPKTYVHSL 180  
 DB 756 KPFSNFISSIQNTKPKNQKFIKVGCLVFRLLANPEGVKYLSEKVIKQIAESL 808

RESULT 4  
 YDH6\_SCHPO  
 ID YDH6\_SCHPO STANDARD: PRT: 1208 AA.  
 AC 092351:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 15-JUL-1998 (rel. 36, Last annotation update)  
 DE HYPOTHETICAL 140.8 KDA PROTEIN C6G9.06C IN CHROMOSOME 1.  
 NC SPAC6G9.06C.  
 CC Schizosaccharomyces pombe (Fission yeast).  
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;  
 CC Schizosaccharomycetaceae; Schizosaccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972:  
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Connor R.E.;  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.

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EMBL: 281317: CAB03608.1: -  
 DR Hypothetical protein; Coiled coil.  
 KM DOMAIN 151 375 COILED COIL (POTENTIAL).  
 FT DOMAIN 387 803 COILED COIL (POTENTIAL).  
 FT DOMAIN 874 1091 COILED COIL (POTENTIAL).  
 FT DOMAIN 1177 1204 COILED COIL (POTENTIAL).  
 SQ SEQUENCE 1208 AA; 140763 MW; 70264159ADD42424 CRC64;

Query Match 8.2%; Score 91.5; DB 1; Length 1208;  
 Best Local Similarity 25.0%; Pred. No. 9.5;  
 Matches 54; Conservative 32; Mismatches 67; Indels 63; Gaps 11;

QY 34 WL-----SVLVSLPQTKVNAESVERIKRRHSQEQTFOLKLMKHONRDOENVKLIK.  
 DB 967 WLERSSTILDESEYRSNOFNON-----NLVODKNLEERLKEIQV--- 1011  
 QY 90 DLCESSV--QRHGHGSLNLTTE--QLALMESLPCKKISPEE-----IERTRTCKSSQEL 140  
 DB 1012 EYVNNHFMQAEIUMSNVTDEQMLKTLRELQSTNNIDHLSLTLENRRKYS-- 1057  
 QY 141 LKLSLW-----RIKNGDQD-----LGLMTALKHLKTSHPKTYVHSLKRT 193  
 DB 1068 --LDDYNOIARARYKNLQNSFTQSGQYSEIEIGLSKLTFRYLOSKCRRE--HSLK 1122  
 QY 184 MRLHSE-----TWYRLQKLFLEMIGNOVQSKIS 214  
 DB 1123 LAFSKFIIIMOLGYETCKNKLRLML---OKIGIS 1154

RESULT 5  
 DNA\_RICPR  
 ID DNA\_RICPR STANDARD: PRT: 463 AA.  
 AC 059758:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 30-MAY-2000 (rel. 39, Last annotation update)  
 DE CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.  
 GN DNAA OR REP601.  
 OS Rickettsia prowazekii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RX MEDLINE-98442214; PubMed-9770078;  
 RA Waite R.T., Shaw E.I., Winkler H.H., Wood D.O.;  
 RT "Isolation and characterization of the dnaA gene of Rickettsia  
 RT prowazekii.";  
 RL Acta Virol. 42:95-101(1998).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RX MEDLINE-99039499; PubMed-9823893;  
 RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,  
 RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.H.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of  
 RT mitochondria.";  
 RL Nature 396:133-140(1998).  
 CC - FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION OF REPLICAT  
 CC OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICAT  
 CC IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS  
 CC (DNAA BOX): 5'-TTATC(C/A)A(C/A)-3'. DNAA BINDS TO ATP AND 1  
 CC ACIDIC PHOSPHOLIPIDS.  
 CC - SIMILARITY: BELONGS TO THE DNAA FAMILY.

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EMBL: U55213: AAA99160.1: -  
 DR EMBL: AJ235272: CAAL5045.1: -  
 DR INTERPRO: IPR001957: -  
 DR PFAM: PF00308: bac\_dnaa. 1.  
 DR PRINTS: PR00051: DNAA.  
 DR PROSITE: PS01008: DNAA. 1.  
 KM DNA replication; DNA-binding; ATP-binding.  
 FT NP\_BIND 168 175 ATP (POTENTIAL).  
 SQ SEQUENCE 463 AA; 53005 MW; F3CA5683DD3B1A1 CRC64;

Query Match 8.18; Score 90; DB 1; Length 463;  
 Best Local Similarity 23.8%; Pred. No. 3.9;  
 Matches 49; Conservative 36; Mismatches 61; Indels 60; Gaps 12;

QY 10 CGIDVTLOEEAFRRVAVFKIIPNLVLY--DISLPGRKVAASEVERIKRR----- 58  
 DB 237 CGKSTQ--EEFPHF--NTLIDNRQWVISCDSRPSLDNIE--DRIKSRIGMGLVADV 290  
 QY 59 HSSOEOTPOLKMKHNRDQEM-----VKRIIDIDCESSVOHILGHSNLT 106  
 DB 291 HST---TTE-LRGLLEKIEQMANVKIPKDVINFLASKIVSNVREGLAKNVIAHSMT 346  
 QY 107 TEOLIALESPLPKKISPEIER-TRTKCKSSQDL-----KLSIMRIKNGDQDTLK 158  
 DB 347 L-----KAITLENTONILRDLRSNERITVEDIOKVASRYNIKLSL----- 389

QY 159 GLMYALKHLKTSHPKTYTHSLRKTM 184  
 DB 390 --MYSRRLREVAPRQIATMYLSKTL 413

RESULT 6  
 CENF\_HUMAN STANDARD; PRT; 3210 AA.  
 ID CENF\_HUMAN P49454; Q13246; Q13171;  
 01-FEB-1996 (Rel. 33, Created)  
 01-FEB-1996 (Rel. 33, Last sequence update)  
 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CENP-F KINETOCHORE PROTEIN (CENTROMERE PROTEIN F) (MITOSIN) (AH ANTIGEN).  
 GN CENP-F.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP TISSUE-BREAST CARCINOMA;  
 RC MEDLINE-95346175; PubMed-7542657;  
 RA Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;  
 RT "CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";  
 RL J. Cell Biol. 130:507-518(1995).  
 RN [2]  
 RP SEQUENCE OF 1-1493 AND 1590-3210 FROM N.A.  
 RC MEDLINE-95379848; PubMed-7651420;  
 RA Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Jones D., Yang-Feng T.L., Lee W.-H.;  
 RT "Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression.";  
 RL Mol. Cell. Biol. 15:5017-5029(1995).  
 RN [3]  
 RP SEQUENCE OF 2194-3210 FROM N.A.  
 RC MEDLINE-95336446; PubMed-7612011;  
 RA Li Q., Ke Y., Karp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;  
 RT "A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for nuclear localization.";  
 RL Biochem. Biophys. Res. Commun. 212:220-228(1995).  
 RN [4]  
 RP CHARACTERIZATION.  
 RC MEDLINE-95370296; PubMed-7642639;  
 RA Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;  
 RT "The C terminus of mitotin is essential for its nuclear localization, centromere/kinetochore targeting, and dimerization.";  
 RL J. Biol. Chem. 270:19545-19550(1995).  
 RN [5]  
 RP CHARACTERIZATION.  
 RC MEDLINE-98437347; PubMed-9763420;  
 RA Chan G.K.T., Schaaf B.T., Yen T.J.;  
 RT "Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBR1.";  
 RL J. Cell Biol. 143:49-63(1998).  
 CC -1- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH

CC RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBR1.  
 CC -1- SUBUNIT: HOMO- OR HETERODIMER.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS).  
 CC REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.  
 CC -1- DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.  
 CC -1- PTM: HYPERPHOSPHORYLATED DURING MITOSIS.  
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DR EMBL; U19769; AAA82889.1; -;  
 DR EMBL; U30872; AAA82935.1; -;  
 DR EMBL; U25725; AAA86889.1; -;  
 DR HSSP; P02649; ILE4.  
 DR MIM; 600236; -;  
 KW Mitosis; Phosphorylation; Antigen; Cell cycle.  
 FT DOMAIN 14 197  
 FT DOMAIN 273 769  
 FT DOMAIN 823 1328  
 FT DOMAIN 1642 1746  
 FT DOMAIN 1862 2987  
 FT DOMAIN 2207 2568  
 FT REPEAT 2207 2386  
 FT REPEAT 2389 2568  
 FT SITE 3015 3032  
 FT CONFLICT 16 16  
 FT CONFLICT 250 250  
 FT CONFLICT 272 272  
 FT CONFLICT 611 611  
 FT CONFLICT 1494 1589  
 FT CONFLICT 1611 1611  
 FT CONFLICT 1811 1811  
 FT CONFLICT 2242 2243  
 FT CONFLICT 2335 2335  
 FT CONFLICT 2492 2492  
 FT CONFLICT 2545 2561  
 SQ SEQUENCE 3210 AA; 367589 MW; 11D83324960E4334 CRC64;

Query Match 7.98; Score 88; DB 1; Length 3210;  
 Best Local Similarity 23.48; Pred. No. 59;  
 Matches 40; Conservative 34; Mismatches 55; Indels 42; Gaps 9;

QY 50 ESVRIKRRHSSOEOTPOL-----KIMKHNRD-----QEWVKI----- 108  
 DB 2618 EISRLKQIDQDQVLSKISQVGEHOLMKQVLELRNLTVLEOKIYQVQSNASID 2677  
 QY 89 -IDCESSVQNRHLGHSNLTTEOLALMESLPGRKISPEIER-----TRTKCKSSQDL 42  
 DB 2678 TLEVLOSSYKYLENELTETKDKKDSFEKVKMKAKTELEOREHNEHMAQTALEDEL 2735  
 QY 143 LLSLMRIKNGDQDTLK-GLYALKHLKTSHP-KTVT---HSLKTYRFLH 188  
 DB 2736 -----SGEKRLAGELQLLLEIKSSKQOLKELTLENSLKSDCMH 2778

RESULT 7  
 RGAL\_YEAST STANDARD; PRT; 1007 AA.  
 ID RGAL\_YEAST P39083; P39934;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE RHO-TYPE GTPASE ACTIVATING PROTEIN RGAL/DBM1.  
 GN RGAL OR DBM1 OR THE1 OR YOR127W OR O3290 OR YOR3290W.

OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.  
 RC STRAIN-S288C;  
 RX MEDLINE-96239492; PubMed-8657111;  
 RA Chen G.-C., Zheng L., Chan C.S.M.;  
 RT "The LIM domain-containing Dbp1 GTPase-activating protein is required  
 for normal cellular morphogenesis in Saccharomyces cerevisiae.";  
 RL Mol. Cell. Biol. 16:1376-1390(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / FY1679;  
 RX MEDLINE-97060020; PubMed-8904341;  
 RA Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vleck C.,  
 Stegmann J., Zimmermann J., Erfle H., Paces V., Ansoerge W.;  
 RT "Sequencing and analysis of 51 kb on the right arm of chromosome XV  
 from Saccharomyces cerevisiae reveals 30 open reading frames.";  
 RL Yeast 12:281-288(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97344368; PubMed-9200815;  
 RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,  
 Schwager C., Paces V., Sander C., Ansoerge W.;  
 RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";  
 RL Yeast 13:655-672(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RX MEDLINE-96101594; PubMed-7498791;  
 RA Stevenson B.J., Ferguson B., de Vargillo C., Bl E., Pringle J.R.,  
 Ammerer G., Sprague G.F. Jr.;  
 RT "Mutation of RGA1, which encodes a putative GTPase-activating protein  
 for the polarity establishment protein Cdc42p, activates the  
 phenome-response pathway in the yeast Saccharomyces cerevisiae.";  
 RL Genes Dev. 9:2949-2963(1995).  
 RN [5]  
 RP SEQUENCE OF 570-639 FROM N.A.  
 RC STRAIN-SNY243;  
 RX MEDLINE-93087574; PubMed-1454852;  
 RA Ramer S.W., Elledge S.J., Davis R.W.;  
 RT "Dominant genetics using a yeast genomic library under the control of  
 a strong inducible promoter.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11589-11593(1992).  
 CC -1- FUNCTION: GTPASE-ACTIVATING PROTEIN (GAP) FOR CDC42 AND/OR RHO1.  
 CC NEGATIVE REGULATOR OF THE PHENOMONE-RESPONSE PATHWAY THROUGH THE  
 CC STE20 PROTEIN KINASE. ACTS AT A STEP BETWEEN THE G-PROTEIN AND THE  
 CC MAP KINASE MODULE. DOMINANT SUPPRESSOR OF BUD EMERGENCE DEFECT  
 CC CAUSED BY DELETION OF IPL2/BEM2. INVOLVED IN THE CONTROL OF  
 CC POLARIZED CELL GROWTH AND PROPER BUD SITE SELECTION.  
 CC -1- SIMILARITY: CONTAINS 1 GAP DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC  
 CC IONS.  
 CC -----  
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 CC -----  
 CC EMBL: U07421; AAA16875.1;  
 DR EMBL: X90518; CA62108.1;  
 DR EMBL: X94335; CA64046.1;  
 DR EMBL: Z73035; CA69326.1;  
 DR EMBL: X90950; CA62445.1;  
 DR EMBL: L02617; AAA35153.1;  
 DR PIR: S48535; S48535;  
 DR SGD: S0005653; RGA1.  
 DR INTERPRO: IPR000198;  
 DR INTERPRO: IPR001781;

DR PFAM: PF00412; LIM; 2.  
 DR PFAM: PF00620; RHO GAP; 1.  
 DR PROSITE: PS00478; LIM DOMAIN 1; 1.  
 DR PROSITE: PS00023; LIM DOMAIN 2; 2.  
 KW GTPase activation; Repeat; LIM motif; Metal-binding; Zinc;  
 KW Phenomone response.  
 FT DOMAIN 13 LIM.  
 FT DOMAIN 70 LIM.  
 FT DOMAIN 122 LIM.  
 FT DOMAIN 805 977 GAP DOMAIN.  
 FT MUTAGEN 40 40 C->S; BIPOLAR BUDDING.  
 FT MUTAGEN 37 37 C->S; BIPOLAR BUDDING.  
 FT MUTAGEN 98 98 C->S; BIPOLAR BUDDING.  
 FT MUTAGEN 101 101 C->S; BIPOLAR BUDDING.  
 FT VARIANT 866 866 V -> A.  
 FT VARIANT 898 898 V -> R.  
 FT VARIANT 926 926 S -> G.  
 FT VARIANT 957 957 D -> E (IN REF. 4).  
 FT CONFLICT 457 457 T -> P (IN REF. 4).  
 FT CONFLICT 507 507  
 SQ SEQUENCE 1007 AA; 112831 MW; C805411B57553791 CRC64;  
 Query Match 7.9%; Score 87.5; DB 1; Length 1007;  
 Best Local Similarity 25.0%; Pred. No. 16;  
 Matches 45; Conservative 25; Mismatches 79; Indels 31; Gaps 9;  
 QY 31 IPNLSVLYDSLPGRKVAESVERIKRRSSQ---EOTFOLKLMKHNRODEWKKI  
 DB 804 IPMLISVCLDFESDEENMRS-EGYRKSGSLVTEIEKOPSAAKVOONTE--TPNII 160  
 QY 88 DIDLCSSVORHLGSHNLTTEOLLALMESLPCKKISPEIERTKCKSSSEOLLK 143  
 DB 861 EDDL-----NVTGVLKRYLKLKLPPIPTFLYEDMLAVSKMMELP 108  
 QY 144 --LSMRKNGD--ODITKGLMTALKHKTSHFP--KTVTHSLKRTMPLH--STFM 195  
 DB 909 GKLSTL-EAKNSDTYSSKSAKLNILEDLPREHYRLVRLSEHIEKVTTRYSHNRTLYNL 967  
 RESULT 8  
 GINA\_YEAST STANDARD: PRT; 1142 AA.  
 ID GINA\_YEAST  
 AC Q12263;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE GINA (EC 2.7.1.-).  
 GN GINA OR YDR507C OR D9719.13.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetaceae;  
 OC Saccharomycetaceae; Saccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99030835; PubMed-9813093;  
 RA Longtine M.S., Fares H., Pringle J.R.;  
 RT "Role of the yeast Gln4p protein kinase in septin assembly and  
 relationship between septin assembly and septin function.";  
 RL J. Cell Biol. 143:719-736(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Ber  
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,  
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin J  
 RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F  
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shoff N.,  
 RA Winant A., Yelton M., Botstein D., Davis R.W.;  
 RL submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MAY PLAY A ROLE IN SEPTIN ASSEMBLY.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASE.  
 CC NIM1 SUBFAMILY.  
 CC -----  
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RA Guerout-Fleury A.M., Gonzy-Treboul G., Stragier P.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / JH642;  
 RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,  
 RA Sato T., Takeuchi M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL: U35252; AAA76726.1; -  
 DR EMBL: D84432; BAA12566.1; -  
 DR EMBL: 299116; CAB14368.1; -  
 DR SUBMITTER: BG11414; SPOTIAC.  
 KW Spotiation; Transmembrane.  
 FT TRANSMEM 30 50  
 FT CONFLICT 14 14  
 FT SEQUENCE 229 AA: 25549 MW: 110310C897BD8691 CRC64;  
 SQ  
 Query Match 7.6%; Score 84.5; DB 1; Length 229;  
 Best Local Similarity 19.0%; Pred. No. 4.6;  
 Matches 34; Conservative 44; Mismatches 48; Indels 53; Gaps 7;  
 Oy 41 SLPGTKVNAESYERIKRRSS--SOEOTFOLKLMK-----HONRDEMYVK 84  
 Db 51 SSEPTEKNAKTTAVSSQSSADSKETAIEYFKASKSDKPKSDIDYEKEYNOLKLETL 110  
 Oy 85 II-----QDIDCESSV-ORHLGHSNLTTEQLALMESLPGRKISPEIERTKTK 135  
 Db 111 IIGVDVSVVAVNDATSLKYERKNKSNKMTTEE-----TDKEGKRSVTDQ 157  
 Oy 136 SFPOLKLLSLMRKRGDDT-----LKGIMYALKHLKTSHPRTVTHSLKTM 184  
 Db 158 SSEEELVW-----TKNGDETPYVOTKKPDIGVLVAQGVNVOIKOTILEAVTRVL 211  
 RESULT 11  
 MYSA\_MOUSE STANDARD; PRT: 1853 AA.  
 AC 099104;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN VA) (MYOSIN 5A).  
 GN MYOSA OR DILUTE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RA MEDLINE-91141583; PubMed-1996138;  
 RA Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,  
 RA Jenkins N.A.;  
 RA "Novel myosin heavy chain encoded by murine dilute coat colour  
 RT locus";  
 RL Nature 349:709-712(1991).  
 RN [2]  
 RP REVISIONS.  
 RA Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,  
 RA Jenkins N.A.;  
 RA Nature 352:547-547(1991).  
 CC -!- FUNCTION: MAY BE INVOLVED IN MELANOSOME TRANSPORT OR  
 CC ALTERNATIVELY, IT MAY BE REQUIRED FOR SOME POLARIZATION PROCESS  
 CC INVOLVED IN DENDRITE FORMATION.

CC -!- SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE  
 CC CALMODULIN OR MYOSIN LIGHT CHAINS.  
 CC -!- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. CLASS-  
 CC MYOSIN SUBFAMILY.  
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 DR EMBL: X57377; CAA0651.1; -  
 DR PIR: A46761; A46761.  
 DR HSSP: P08799; 1MND.  
 DR MGD: MGI:105976; MYOSA.  
 DR INTERPRO: IPR000048; -  
 DR INTERPRO: IPR001609; -  
 DR INTERPRO: IPR002710; -  
 DR PFAM: PF01843; DIL; 1.  
 DR PFAM: PF00612; IO; 6.  
 DR PFAM: PF00063; myosin\_head; 1.  
 DR PRINTS: PRO0193; MYOSINHEAVY.  
 KW Myosin; Repeat; ATP-binding; calmodulin-binding; actin-binding;  
 KW Coiled coil; Phosphorylation.  
 FT DOMAIN 1 765  
 FT DOMAIN 766 913  
 FT DOMAIN 914 1040  
 FT DOMAIN 1041 1853  
 FT DOMAIN 643 665  
 FT DOMAIN 766 887  
 FT REPEAT 766 790  
 FT REPEAT 791 815  
 FT REPEAT 816 837  
 FT REPEAT 838 863  
 FT REPEAT 864 888  
 FT DOMAIN 773 787  
 FT DOMAIN 796 810  
 FT DOMAIN 821 835  
 FT DOMAIN 844 862  
 FT DOMAIN 869 884  
 FT DOMAIN 892 906  
 FT NP BIND 163 170  
 FT MOD RES 1758 1758  
 FT SEQUENCE 1853 AA: 215594 MW: 503E93D48CA6B766 CRC64;  
 SQ  
 Query Match 7.5%; Score 83.5; DB 1; Length 1853;  
 Best Local Similarity 24.5%; Pred. No. 69;  
 Matches 27; Conservative 25; Mismatches 35; Indels 23;  
 Oy 46 KYNAESYERIKRRSSOE-QTFOLKLMKHONRDEMV-----KRILQ 99  
 Db 909 KIEARSVERKRLHGMENKIMQLORVDEQNKDKYKCLMEKLTNLEGVYNSETEKLRNI 1008  
 Oy 90 DICESSVQRHLGHSNLTTEQLALMESLPGRKISPEIERTKTKSSQ 139  
 Db 969 ERLQSEE---EAVVATGRVLSLOEETAKLR--KLEQTRSEKRSIEE 1011  
 RESULT 12  
 SMC3\_YEAST STANDARD; PRT: 1230 AA.  
 AC P47037;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CHROMOSOME SEGREGATION PROTEIN SMC3 (DA-BOX PROTEIN SMC3).  
 GN SMC3 OR YJL074C OR J1049.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetaceae;  
 OC Saccharomycetaceae; Saccharomycetes.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-W303;  
 RX MEDLINE=9747309; PubMed=9335333;  
 RA Michaelis C., Ciosk R., Nasmyth K.;  
 RT "Cohesins: chromosomal proteins that prevent premature separation of  
 sister chromatids."  
 RL Cell 91:35-45(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Koeltter P., Entian K.D.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RA Sor F.J.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD BE  
 CC PART OF A CHROMOSOME CONDENSATION MOTOR.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
 CC -1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS  
 CC FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.  
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Y14278; CAAT4655.1; -  
 DR EMBL: 249349; CAAB9366.1; -  
 DR EMBL: X88851; CAA61313.1; -  
 DR SGG: S0003610; SMC3.  
 KM Mitosis; ATP-binding; Coiled coil; Nuclear protein.  
 FT NP\_BIND 32 39 ATP (POTENTIAL).  
 FT DOMAIN 172 482 COILED COIL (POTENTIAL).  
 FT DOMAIN 685 1041 COILED COIL (POTENTIAL).  
 FT SEQUENCE 1230 AA; 141336 MW; B152D88F780341F CRC64;  
 SQ  
 Query Match 7.5%; Score 83; DB 1; Length 1230;  
 Best Local Similarity 21.6%; Pred. No. 46;  
 Matches 43; Conservative 35; Mismatches 65; Indels 56; Gaps 11;  
 QY 38 LVDSL--PGTVNAESV-----RIKRHSQEQTFOLKLMKHONRODMVKKIIOIDIL 91  
 Db 445 LIDINGPDTGOLEDPESELIHKOKLSESLDTRK--ELMRKQKLTQVLETLSDVQ 502  
 QY 92 CESSVORHLGHSNLTTEBOLLALMESLPKGISPEIERT-----RKTCK----- 135  
 Db 503 NORVNVETMS--LANCIIVKTEKLTSPESVFTGLCELKLVNDKYTCAEVIGCN 560  
 QY 136 -----SSQDLKLK--SLMRKNG-----DOD-----TLKGLMYA--LKH 166  
 Db 561 SLFHVVDTEETATLIMELRYKMGKGVTFIPLNRLSLDSVKKPSNTTQIQFTPLKK 620  
 QY 167 LK-TSHPKTYTHSLRKT 184  
 Db 621 IKYPRFEKAVHVGKTI 639  
 RESULT 13  
 RBP2\_PLAVB STANDARD; PRT; 1251 AA.  
 AC 000799;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).  
 GN RBP2.

OS Plasmodium vivax (strain Belem).  
 NC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9231538; PubMed=1617731;  
 RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;  
 RT "A reticulocyte-binding protein complex of Plasmodium vivax  
 merozoites."  
 RL Cell 69:1213-1226(1992).  
 CC -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO  
 CC HUMAN RETICULOCYTE CELLS.  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).  
 CC -----  
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 CC -----  
 DR EMBL: M88098; AAA29744.1; -  
 KM Malaria; Receptor; Membrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;  
 Query Match 7.5%; Score 83; DB 1; Length 1251;  
 Best Local Similarity 24.1%; Pred. No. 47;  
 Matches 38; Conservative 32; Mismatches 50; Indels 38; Gaps 7;  
 QY 39 VDSLPGTGVNAESVRIKRHSQEQTFOLK--LMKHONRODMVKKIIOIDILDCS 1  
 Db 954 IDSL-----MTADELLKKGKTCVSKRKIKDVTVEISDTELTMT-----EKNF 401  
 QY 97 QRHLGHSNLT--TEEDLALMESLPKGISPEIERTKTKSSQDLKLKLS-----LV 147  
 Db 1002 KAVLAYIKKNVEDVQVLTLEHFNTRKQVNSHEPTNEDKSNKSEELTAVTDSKTI 1061  
 QY 148 RIK-----NGQDF-----LKGLMYALKLKTS 170  
 Db 1062 KIKGVILVENMENTEMNTSSAKIEALYNELNKRKTS 1099  
 RESULT 14  
 PCNT\_MOUSE STANDARD; PRT; 1920 AA.  
 AC P48725;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE PERICENTRIN.  
 GN PCNT.  
 OS Mus musculus (Mouse).  
 NC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170365; PubMed=8124707;  
 RA Doherty S.J., Stein P., Evans L., Calarco P.D., Kirschner M.;  
 RT "Pericentrin, a highly conserved centrosome protein involved in  
 RT microtubule organization."  
 RL Cell 76:639-650(1994).  
 CC -1- FUNCTION: INTEGRAL COMPONENT OF THE FILAMENTOUS MATRIX OF THE  
 CC CENTROSOME INVOLVED IN THE INITIAL ESTABLISHMENT OF ORGANIZING  
 CC MICROTUBULE ARRAYS IN BOTH MITOSIS AND MEIOSIS.  
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN KIDNEY, THYMUS,  
 CC LIVER, LOW LEVELS IN BRAIN, MUSCLE, LUNG AND HEART.  
 CC -1- DOMAIN: COMPOSED OF A COILED-COIL CENTRAL REGION FLANKED BY  
 CC HELICAL N- AND C-TERMINALS.  
 CC -1- SIMILARITY: STRONG, TO HUMAN KENDRIN.



```

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CC      -----
DR      EMBL; U05823; AAA17866.1; -.
DR      MGD; MGI:102722; PCNT.
KW      Coiled coil; Microtubules.
KW      DOMAIN 110 1600 COILED COIL (POTENTIAL).
FT      DOMAIN 109 112 POLY-PRO.
FT      DOMAIN 383 387 POLY-GLN.
FT      SEQUENCE 1920 AA; 218337 MW; CF1DD0ADEC5B73309 CRC64;
Query Match 7.5%; Score 83; DB 1; Length 1920;
Best Local Similarity 22.5%; Pred. No. 79;
Matches 42; Conservative 35; Mismatches 86; Indels 24; Gaps 6;
QY      5 EATQKCGIDVTLCEAEFR-----FAVPTKIIPMWLSYVDSLPSTKV-NAESVERIKR 57
DQ      1002 ETSVCEISSHVCSEFIRPENTLDCQDPIRVYQSLSTAVAGLLEMLDSSKQLEAPK 1061
QY      58 RHSSQEQIFOLLKLKKHNRQDQEWKKTIIQIDIDCESSQVRHLGHSNLTTEOLLAMESL 117
DQ      1062 LHRQVEERF-----RRRNEEMQAMQKQOELLERLRSESAARDRLAE-LHTAKGL 1112
QY      118 PGKRTSPFEIRTRKTSQSEOLLKLKLSMRKNGDOPTLKLKALYKLKTSHPKPYT 177
DQ      1113 EGFKEKVDLQALQKKESEQQL-ILEL-----EDLRKQLEQARALLTLKEKSVL 1164
QY      178 HSLRRTM 184
DQ      1165 WNKQETL 1171
RESULT 15
ACVS_CEPAC STANDARD: PRT; 3712 AA.
AC AC P25464;
CT 01-MAY-1992 (Rel. 22, Created)
CT 01-MAY-1992 (Rel. 22, Last sequence update)
CT 15-JUL-1998 (Rel. 36, Last annotation update)
DE DELTA-L-L-ALPHA-AMINOADIPYL-L-CYSTEINYL-D-VALINE SYNTHETASE
DE (EC 6.-.-.-) (ACV SYNTHETASE) (ACVS).
GN PCBAB.
OS Cephalosporium acremonium (Acremonium chrysogenum).
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Acremonium.
RN [1]
RN RP MEDLINE-91177827; PubMed-1706706;
RX Gutierrez S., Diez B., Montenegro E., Martin J.F.;
RX "Characterization of the Cephalosporium acremonium pcbAB gene
RX encoding alpha-aminoadipyl-L-cysteinyl-valine synthetase, a large
RX multidomain peptide synthetase: linkage to the pcbC gene as a cluster
RX of early cephalosporin biosynthetic genes and evidence of multiple
RX functional domains";
RX J. Bacteriol. 173:2354-2365(1991).
RN [2]
RN RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RN RC STRAIN-ATCC 11550;
RX MEDLINE-91168300; PubMed-2076552;
RX Hoskins J.A., O'Callaghan N., Queener S.W., Cantwell C.A., Wood J.S.,
RX Chen V.J., Skatrud P.L.;
RX "Gene disruption of the pcbAB gene encoding ACV synthetase in
RX Cephalosporium acremonium.";
RX Curr. Genet. 18:523-530(1990).
CC -1- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE
CC ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PEPTIDE BONDS
CC FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER
CC INTERMEDIATES.

```

CC	-1	COFACTORS: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANETHEINES (POTENTIAL)
CC	-1	PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND CEPHALOSPORIN.
CC	-1	SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
CC		PIR: A38511; YGCEVC.
DR		HSSP: P14687; 1AMU.
DR		INTERPRO: IPR000255; -.
DR		INTERPRO: IPR000873; -.
DR		INTERPRO: IPR001031; -.
DR		INTERPRO: IPR001242; -.
DR		PFAM: PF00501; AMP-binding; 3.
DR		PFAM: PF00668; DUF4; 3.
DR		PFAM: PF00975; Thioesterase; 1.
DR		PFAM: PF00550; pp-binding; 3.
DR		PRINTS: PR00154; AMBANDING.
DR		PROSITE: PS00012; PHOSPHOPANETHEINE; 2.
DR		PROSITE: PS00455; AMP BINDING; 3.
DR		PROSITE: PS50075; ACP-DOMAIN; 3.
KW		Ligase: Antibiotic biosynthesis; Multifunctional enzyme.
KW	Repeat:	Phosphopantetheine.
FT	Repeat	234 1062
FT	Repeat	1335 2162
FT	Repeat	2409 3387
FT	DOMAIN	795 864
FT	DOMAIN	1880 1953
FT	DOMAIN	2960 3027
FT	BINDING	827 827
FT	BINDING	1916 1916
FT	BINDING	2890 2990
FT	ACT_SITE	3568 3568
SO	SEQUENCE	3712 AA: 144767 MW: 468315556EF987 CR664: THIOESTERASE (BY SIMILARITY).

```

Query Match      7.5%  Score 83  DB 1:  Length 3712;
Best Local Similarity 23.5%  Pred. No. 1,8e+02;
Matches 46;  Conservative 35;  Mismatches 85;  Indels 30;
OY  14  VTLCSEAFRRFAVPKTI-----IPMWLSVLD--SLPGTVKMAESVERIKRRHSSEQ 16
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db   739  LSELEKLPYRMYPTVLOAIPINIGKADLRALPAVEAAVAPPHKDDGERGNOLA 740
OY  67  QLLKIMKHNRQDEWKIITDIDICSESSVRHGHGHNLTEDDLMLMESLPGRKISPER 120
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db   798  DLAIAMGN-----IISVPAQDIG--SESNFRLLGSH--IACIOLIAVRQQLGSGITIT 800
OY  127 IERTRTKSSSEDLKLKLSLWRIRKNGDODTLKGLMVALIKHLKHTSHPPT----- 130
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db   850  VFQF--KTLRMAALLS--EKYTKASNGTNGVNGTAHVNGHAANGCHSDSVYASSLQGG 855
OY  177 THSLKTRMRLHSFTM 192
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db   908  YHSLKLNELS--EAYTM 921
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

Search completed: January 27, 2001, 11:24:56  
Job time: 138 sec

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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:37 ; Search time 25.38 seconds  
(without alignments)  
577.878 Million cell updates/sec

Title: US-09-389-545-2.COPY\_186\_401  
Perfect score: 1113  
Sequence: 1 GGNREXQKCGIDVTLCSEA.....OKLFLEMIGNQGVSKISCL 216  
Working table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR-66:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	9.0	1574	1 A38454	myosin MYO2 - yeast
2	95.5	8.6	697	2 T37827	hypothetical prote
3	95	8.5	203	2 T1488	MADS-box protein d
4	95	8.5	486	2 T21481	hypothetical prote
5	92	8.3	1309	2 T39379	sexual differentiation
6	91.5	8.2	901	2 JC7111	tetratricopeptide
7	91.5	8.2	1208	2 T39068	coiled coil protei
8	91	8.2	1364	2 T14900	condensin XCAP-D2
9	90.5	8.1	463	2 T32289	hypothetical prote
10	90	8.1	463	2 C71665	chromosomal replic
11	88.5	8.0	710	2 T22360	hypothetical prote
12	88.5	8.0	1388	2 T30335	KIP2 protein - Afr
13	88	7.9	361	2 T50691	basic-leucine zipp
14	88	7.9	523	2 T19684	hypothetical prote
15	88	7.9	1017	2 PC4035	cell-cycle-depende
16	88	7.9	1225	2 A56514	chromokinesin - ch
17	87.5	7.9	1007	2 S48535	rho-type GTPase-ac
18	87	7.8	823	2 D70386	probable polyketid
19	87	7.8	1215	2 B72029	helicase, Sfr2/Rad
20	87	7.8	4151	2 T13734	groovin gene prote
21	86.5	7.8	1142	2 S59359	GN4 protein - yea
22	86	7.7	1442	2 C82888	DNA polymerase III
23	86	7.7	1837	2 T41023	probable nuclear p
24	86	7.7	2677	2 A38194	desmoplakin I - hu
25	84.5	7.6	229	2 B69712	mutants block spor
26	84.5	7.6	764	2 T51302	myosin heavy chain
27	84.5	7.6	812	2 A53016	myosin heavy chain
28	84	7.5	451	2 T21036	hypothetical prote
29	84	7.5	1226	2 I51617	kinesin-like prote

30	83.5	7.5	1853	1 A46761	myosin heavy chain
31	83.5	7.5	2018	2 T34274	hypothetical prote
32	83	7.5	817	2 T25674	hypothetical prote
33	83	7.5	1230	2 S56850	SMC1 protein homol
34	83	7.5	1252	2 B42771	reticulocyte-Dnbl1
35	83	7.5	1920	2 A53188	pericenturin - mous
36	83	7.5	3712	1 YGCEVC	alpha-aminoadipyl-
37	82.5	7.4	1330	2 A36373	hypothetical prote
38	82.5	7.4	3450	2 T26863	hypothetical prote
39	82	7.4	152	2 S42855	viral integrase
40	82	7.4	370	2 B70223	conserved protein
41	82	7.4	435	2 S67205	probable proteinase
42	81.5	7.3	395	2 B64709	transcriptase term
43	81.5	7.3	395	2 T19365	transcription term
44	81.5	7.3	530	2 T19365	hypothetical prote
45	81.5	7.3	682	2 S40459	ribosomal protein

## ALIGNMENTS

RESULT 1  
A38454  
myosin MYO2 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein O6167; protein YOR326w  
C:Contents: myosin ATPase (EC 3.6.1.32)  
C:Species: Saccharomyces cerevisiae  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-1-2000  
C:Accession: A38454; S58339; S62058; S67232; S67233; S71966; S72005  
R:Johnston, G.C.; Prendergast, J.A.; Singer, R.A.  
J. Cell Biol. 113, 539-551, 1991  
A:Title: The Saccharomyces cerevisiae MYO2 gene encodes an essential protein for vecto  
A:Reference number: A38454; MIMD:91201404  
A:Accession: A38454  
A:Molecule type: DNA  
A:Residues: 1-1574 <JON>  
A:Cross-references: GB:M35532; NID:q172021; PIDN:AAA34810.1; PID:q17.  
R:Pearson, B.M.; Hernandez, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweitzer, M.  
submitted to the EMBL data library, August 1995  
A:Reference number: S58339  
A:Accession: S58339  
A:Molecule type: DNA  
A:Residues: 1-748 <PEA>  
A:Cross-references: EMBL:X00565; NID:q940836; PIDN:CAA62184.1; PID:q94.000  
R:Parle, A.G.; Hand, N.J.; Goulding, S.G.; Wolfe, K.H.  
submitted to the EMBL data library, June 1995  
A:Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sa  
A:Reference number: S62058  
A:Accession: S62058  
A:Molecule type: DNA  
A:Residues: 677-1574 <PAR>  
A:Cross-references: EMBL:Z49821; NID:g1163062; PIDN:CAA89973.1; PID:q17063  
R:Pearson, B.M.; Hernandez, Y.; Kalogeropoulos, A.; Schweitzer, M.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67213  
A:Accession: S67213  
A:Molecule type: DNA  
A:Residues: 1-748 <PEW>  
A:Cross-references: EMBL:Z75234; GSPDB:GN00015; MIPS:YOR326w  
R:Goulding, S.E.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67233  
A:Accession: S67233  
A:Molecule type: DNA  
A:Residues: 677-1574 <GOU>  
A:Cross-references: EMBL:Z75234; GSPDB:GN00015; MIPS:YOR326w  
R:Parle-McDermott, A.G.; Hand, N.J.; Goulding, S.E.; Wolfe, K.H.  
Yeast 12, 999-1004, 1996  
A:Title: Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces c  
A:Reference number: S71966; MIMD:97051586  
A:Accession: S71966





Db 967 WLEBERSILDELBSYSNOFNON-----NLVODKNELERLEKEIKEL 1011  
 Oy 90 DLCESSV--QRHLGHSNLTTE---QLALMESLPCKRISPE-----LERTKCTCKSSQOL 140  
 Db 1012 EYNNHMKQALMTSNVTDSQMLKTLREALOSKTNNDHLSTILERNKREYS----- 1067  
 Oy 141 LKLISLW-----RIKNGDQDT-----LKLWYALKHLKTSHPPTVTHSLRKT 183  
 Db 1068 --LDDYQNLARKNLQSNPNQSQGYSEIKGLSKLRYLQSKCRRE---HSLJLD 1122  
 Oy 184 MRLHSF-----TWRLYOKLFLEKIGNOVOSKIS 214  
 Db 1123 LAFSKRFLMQLTGYETCNKINLRML---OKIGIS 1154

RESULT 8  
 T14900  
 condensin XCAP-D2 chain - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 11-May-2000  
 C:Accession: T14900  
 R:Kimura, K.; Hirano, M.; Kobayashi, R.; Hirano, T.  
 Science 282:487-490, 1998  
 A:Title: Phosphorylation and activation of 13S condensin by cdc2 in vitro.  
 Reference number: Z18257; MUID:98447791  
 C:Accession: T14900  
 A:Title: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1364 <KIM>  
 A:Cross-references: EMBL:AF067969; NID:g3764086; PID:g3764087; PIDN:AC64359.1

Query Match 8.2%; Score 91; DB 2; Length 1364;  
 Best Local Similarity 20.8%; Pred. NO. 34;  
 Matches 54; Conservative 34; Mismatches 68; Indels 104; Gaps 10;

Oy 4 REATQKCGIDVTLCBEAFERRA-----VPRKIIPNMLSVLVSPLPGTK----- 46  
 Db 276 REIGQKCGQDLSRESSGKFAFETLELAEERIPALMPS-LSVLIDYDGENYMMRNSVL 334  
 Oy 47 -VNAESVRI-----KRRHSSQOTFOLKMKHQ----- 75  
 Db 335 TWGMGVAVRVLSGQLEAEKSSKQPLDTLQEHLDVNTYVRSVCVQIYNRIYOEKALP 394  
 Oy 76 -NRDQEMVKIIT---ODIDLCSSVQ---RHLGHSNLT-----TEQLL 111  
 Db 395 LSRFSVVTIVVGRFLDQSVAVCKNAIQLLASFLANNPFTCKLSVDLKVLEKRTKXK 454  
 Oy 112 ALMESLPCKR---ISPE-----ELERTKCTCKSSQOL 140  
 Db 455 EMREKYQCPKPVVVISPEEWEAMLPEVLEAFKILQESKEEDEIETEEISSQHLRQOI 514  
 Oy 141 LKLISLWIKKNGDQDTLKL 160  
 Db 515 LILLKRTSYKNSIRLTOKGI 534

RESULT 9  
 T32289  
 hypothetical protein F4262.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T32289  
 R:Schaeft, P.; Maggi, L.  
 submitted to the EMBL Data Library, September 1997  
 A:Description: The sequence of C. elegans cosmid F4262.  
 A:Reference number: Z21146  
 C:Accession: T32289  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-833 <SCH>  
 A:Cross-references: EMBL:AF024499; PIDN:AAV0358.1; GSPDB:GN00020; CESP:F4262.6  
 A:Experimental source: strain Bristol N2; clone F4262

C:Genetics:  
 A:Gene: CESP:F4262.6  
 A:Map position: 2  
 A:Introns: 317/1; 335/1; 362/3; 781/1

Query Match 8.1%; Score 90.5; DB 2; Length 833;  
 Best Local Similarity 29.7%; Pred. No. 21;  
 Matches 33; Conservative 17; Mismatches 42; Indels 19; Gaps 4;

Oy 54 RIKRRHSSQEQTFOLKLV-KHQRDQEMVKIITODIDLCSSVQRL----- 100  
 Db 679 RKKLRMSKRQNELLOLWELKENTENTHAEKTNQEKLENNVOEQLQEMMKRQIEEP 738  
 Oy 101 -GHSNLTTEQL-LALMESLPCKRISPEEIE---RTRKCTCKSSQOLKILS 145  
 Db 739 AADSKNLKLEQWVLEMDKIDDAQETRIKELEEVYKSKNNAKKGEOULDLS 789

RESULT 10  
 C71665  
 chromosomal replication initiator protein dnaa (dnaa) Rp601 - Rickettsia prowazekii  
 C:Species: Rickettsia prowazekii  
 C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 20-Jun 2000  
 C:Accession: C71665  
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Poulsen, T.; Alsmark  
 Nature 396:133-140, 1998  
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria  
 Reference number: A71630; MUID:99039499  
 A:Accession: C71665  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-463 <AND>  
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAV1 1.1; PID:g386  
 A:Experimental source: strain Madrid E  
 C:Genetics:  
 A:Gene: dnaa; Rp601  
 C:Superfamily: replication initiation protein dnaa

Query Match 8.1%; Score 90; DB 2; Length 463;  
 Best Local Similarity 23.8%; Pred. NO. 12;  
 Matches 49; Conservative 36; Mismatches 61; Indels 60; Gaps 12;

Oy 10 CGIVTLCBEAFERRAFTKIIPNMLSVLV--DSLPTKYNAESVERIKRR----- 148  
 Db 237 CGKQSTQ-EEFFHTF---NLLIDNNRQWVISCDSKPSDDNIE--DRIKSRLEMGVLAIV 290  
 Oy 59 HSSQEQTFOLKLVKHQRDQEM-----VKIITODIDLCSSVQRLGHSNLT 106  
 Db 291 HST---TYE-LRLGILTSKIEQMWVKIPKDVINFLASKIVSNVRELGAANKVIAHSNF 146  
 Oy 107 TEQLALMESLPCKRISPEEIER-TRKCTCKSSQOL-----KLISLWIKKNGDQDT 158  
 Db 347 L-----KATLENTQNLRLDLSRNEIIVEDIQKVASRYNIKUSD----- 189  
 Oy 159 GLWYALKHLKTSHPKTVTHSLRKT 184  
 Db 390 --WTSRRLREVARPRQIAYLSKTL 413

RESULT 11  
 T22360  
 hypothetical protein F4764.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T22360  
 R:White, S.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z19553  
 C:Accession: T22360  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

RESULT 13  
150691

Db	355	-ELSEQIKKIQLKDRQNVKREIDLEDLKEIGRKSVLSTEVEMAKIFDENYQIV
Qy	186	FLHSFTMYRLYQKL 199

```

      .      |::|||:|
Db 414  ALNAGPMYNLQENL 427

```

## RESULT 15

PC4035

cell-cycle-dependent 350K nuclear protein - human (fragment)

C;Species: Homo sapiens (man)

C:\Accession: PCA025  
C:\Date: 08-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000

C;Accession: PC4035  
P.T.I. O : ka V : k

R; Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshl, H.C.  
Biochem Biophys Res Commun 212:220-228, 1995

**A·Title:** A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for

A:Reference number: PC4035; MUID:95336446

A: Accession: PC4035

A:Molecule type: DN

A;Residues: 1-1017 <

A; Cross-references: GB:U

A;Note: repeat 15-160 and 200-340

C;Comment: This protein contains

**Keywords:** nucleoprotein; phosphoprotein

F;465/Binding site: phosphate (Thr) (cova

F;825,826,838/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status

F;908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pr

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

Query match	7.98;	Score 88;	DB 2;	Length 1017;
-------------	-------	-----------	-------	--------------

Best Local Similarity 23.48; Pred. No. 41;

Matches	40;	Conservative	34;	Mismatches	55;	Indels	42;	Gaps	9;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

QY 50 ESVERIKRRHSSQEQTFOLL-----KLWKHQNRD-----QEMVKKI-----IQD 88

Db 425 EEISRLKNIQDQEQLVSKLSQVEGEHQWLWKEQNLELRLNLTVELLEQKIQVLQSKNASLQD 484

QY 89 - IDLCSSVQRHLGHSNLTTEQLLALMESLPKKISPEIER-----TRKTKCSSEQLLK 142

Db 485 TLEVLQSSYKNLELELT KMDKMSFEVEKVNKMTAKETELQREHHEMAQKTAELQEEEL - - 542

QY 143 LLSLWRIKNGDQDTLKG-LMYALKHLKTSHER-KTVT---HSLRKTMRFLH 188

Db 543 -----SGEKNRLAGELQLLLEIKSSKDQLKELTLENSELKSLDCMH 585

Search completed: January 27, 2001, 11:23:12  
Job time: 35 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:38 ; Search time 32.57 Seconds

226.769 Million cell updates/sec

```

Title:      US-09-389-545-2_COPY_186_401
Perfect score: 1113
Sequence:   1 SGNREATQRCGIDVTLCEA.....QKLEFMIGNQVQSVKISCL 216

```

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing:	Minimum Match 08
	Maximum Match 100%

### Listing first 45 summaries

Database :

A\_Geneseq\_36: \*

1:	/SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT *
2:	/SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT *
3:	/SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT *
4:	/SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT *
5:	/SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT *
6:	/SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT *
7:	/SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT *
8:	/SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT *
9:	/SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT *
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12:	/SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT *
13:	/SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT *
14:	/SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT *
15:	/SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT *
16:	/SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT *
17:	/SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT *
18:	/SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT *
19:	/SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT *
20:	/SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT *
21:	/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100.0	401	18	W83834		Mouse osteoproteger
2	1073	96.4	208	20	W89231	Mouse osteoprotege
3	1069	96.0	401	18	W83433	Rat osteoprotegeril
4	1029	92.5	208	20	W89230	Rat osteoprotegerin
5	977	87.8	360	17	R89936	Mutated OCIF, OCIF
6	977	87.8	380	17	R39924	Matuere osteoclasto
7	977	87.8	391	19	W53238	Human OCIF genome
8	977	87.8	401	17	R99925	Full length osteoc
9	977	87.8	401	19	W53239	Human OCIF genome
10	977	87.8	401	20	Y05742	Tumour necrosis fa
11	977	87.8	401	20	W85030	Tumour necrosis fa
12	977	87.8	401	20	W83926	Human FTHMA-070 pr

13	972	87.3	359	17	W59395
14	972	87.3	401	19	W56355
15	969	87.1	401	18	W28385
16	969	87.1	401	21	Y43400
17	967	88.9	359	17	R793939
18	967	88.9	401	17	R993932
19	967	88.9	401	17	R993935
20	967	88.9	401	17	R993931
21	964	86.6	399	17	R993933
22	964	86.6	401	17	R993933
23	962	86.4	401	17	R993934
24	960	86.3	360	17	R993938
25	949	85.3	420	20	W892244
26	946	85.0	208	20	W892323
27	932	83.7	417	20	W892266
28	931	83.6	393	17	R993968
29	929	83.5	395	19	W57636
30	833	74.8	397	20	W89327
31	779.5	70.0	390	17	R99337
32	749	67.3	351	17	R99353
33	695.5	62.5	366	20	W892288
34	621	55.8	327	17	R993941
35	592	53.2	321	17	R993940
36	565.5	51.2	326	17	R993940
37	558.5	50.2	349	20	W83928
38	446.5	40.1	311	20	W893229
39	416	37.4	272	17	R993944
40	100	9.0	590	21	Y83080
41	91.5	8.2	228	20	Y258965
42	89	8.0	3248	17	R993786
43	88	7.9	2482	16	R72826
44	88	7.9	2482	16	R72826
45	86	7.7	1752	20	Y07031

## ALIGNMENTS

RESULT	1
W838344	
ID	W838344 standard; Protein; 401 AA.
XX	
AC	W838344;
XX	
DT	20-APR-1998 (first entry)
XX	
DE	Mouse osteoprotegerin.
XX	
KM	Osteoprotegerin; antibody; diagnosis; affi-
KM	recombinant production; transgenic animal
KM	antisense oligonucleotide; probe; detect
KM	bone disease; osteoporosis; Paget's disea
KM	hyperparathyroidism; rheumatoid arthriti
KM	osteolytic metastasis; periodontal bone l
KM	osteopaenia; murine.
XX	
OS	Mus sp.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	90..1295
FT	/tag= a
FT	/product= osteoprotegerin
XX	
PN	DE19654610-A1.
XX	
PD	26-JUN-1997.
XX	
PF	20-DEC-1996;
XX	96DE-1054610.
XX	
PR	03-SEP-1996;
XX	96US-0706945.
PR	22-DEC-1995;
XX	95US-0577788.
XX	
PA	(AMGE-) AMGEN INC

[illegible]

XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;  
 XX WPI: 1997-334271/31.  
 DR N-PSDB; T96062.  
 XX

PT Nucleic acid encoding osteoprotegerin - useful for treatment of  
 PT diseases involving excessive bone loss, e.g. osteoporosis  
 XX  
 PS Claim 23; Pages 106-107; 182pp; German.

XX The present sequence is mouse osteoprotegerin (OPG). Anti-OPG  
 CC antibodies can be used in OPG diagnostic assays, and as affinity  
 CC purification materials. The OPG cDNA can be used to express  
 CC recombinant OPG and to generate transgenic animals. It can also  
 CC be used to regulate the level of OPG in mammals, specifically to  
 CC increase OPG levels, however the use of antisense sequences is  
 CC also contemplated. Fragments of the cDNA can be used as probes to  
 CC detect OPG expressing cells and tissue, and to screen cDNA  
 CC libraries for related sequences. OPG can be used to treat or  
 CC prevent bone diseases, specifically excessive bone loss, e.g.  
 CC osteoporosis, Paget's disease, hypercalcaemia,  
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,  
 CC osteolytic metastases, periodontal bone loss, bone necrosis and  
 CC osteopaenia.

XX Sequence 401 AA;

Query Match 100.0%; Score 1113; DB 18; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-107;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGNRATQKCGIDVTLCEAFRFAVPTKIIPNMLSVLVDSLPGRVNAESVERIKRRHS 60  
 Db 186 sgnreaqkcgidvltlceafrrfapvtpkllpnwlsvlvdsipgkvaesverikrrhs 245  
 OY 61 SOEQTFOLKILMKHONRDOEMVKIITODIDCESSVQRHLSNLTTEQLALMESLPK 120  
 Db 246 sqeqtfqlklwkhqnrqemwkkliqdidcessvqrhlsnltteqlalmeslpk 305  
 OY 121 KISPEIRTRKTKCKSSQQLKLKLSMRKNGDDOTLGLMVALKHLKTSHPKTVTHSL 180  
 Db 306 kispelerttrtkckssqqlklklsmrkngddotlglmyalkhlktshtpvtvthsl 365  
 OY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216  
 Db 366 rktmrflhsftmyrlyqkflflemignovsvkiscsl 401

RESULT 2  
 W89231  
 TD W89231 standard; Protein; 208 AA.

XX W89231;

XX 04-MAR-1999 (first entry)

XX Mouse osteoprotegerin dimerisation domain.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.

XX Mus sp.

XX W09849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98MO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI: 1999-034661/03.

PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders

XX Disclosure; Fig 1; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents mouse OPG dimerisation domain.

XX Sequence 208 AA;

Query Match 96.4%; Score 1073; DB 20; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-103;  
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 KCGIDVTLCEAFRFAVPTKIIPNMLSVLVDSLPGRVNAESVERIKRRHSOQTFOL 68  
 Db 1 kcgidvltlceafrrfapvtpkllpnwlsvlvdsipgkvaesverikrrhsqeqtfql 60  
 OY 69 LKMKHONRDOEMVKIITODIDCESSVQRHLSNLTTEQLALMESLPKTSPEEIF 128  
 Db 61 lkwhqnrqemwkkliqdidcessvqrhlsnltteqlalmeslpktspeei 120  
 OY 129 RTRKTKSSQQLKLKLSMRKNGDDOTLGLMVALKHLKTSHPKTVTHSLRKTMRFL 188  
 Db 121 rtrtkckssqqlklklsmrkngddotlglmyalkhlktshtpvtvthslrktmrfl 180  
 OY 189 SFTMYRLYOKLFLEMIGNOVSVKISCL 216  
 Db 181 sftmyrlyqkflflemignovsvkiscsl 208

RESULT 3  
 W38343  
 ID W38343 standard; Protein; 401 AA.

XX W38343;

XX 20-APR-1998 (first entry)

XX Rat osteoprotegerin.

XX Rat; osteoprotegerin; antibody; diagnosis; affinity purification;  
 KW recombinant production; transgenic animal; treatment; prevention;  
 KW antisense oligonucleotide; probe; detection; screening;  
 KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;  
 KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;  
 KW osteolytic metastasis; periodontal bone loss; bone necrosis;  
 KW osteopaenia.

XX Rat sp.

XX Rattus sp.

XX

XX

PN DE19654610-A1.  
 XX  
 PD 26-JUN-1997.  
 XX  
 PF 20-DEC-1996; 96DE-1054610.  
 XX  
 PR 03-SEP-1996; 96US-0706945.  
 PR 22-DEC-1995; 95US-0577788.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Calzone FJ, Lacey DL, Chang MS;  
 DR WPI; 1997-334271/31.  
 DR N-PSDB; T96061.  
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of  
 XX diseases involving excessive bone loss, e.g. osteoporosis  
 PS  
 XX Claim 23; Pages 102-104; 182pp; German.  
 CC The present sequence is rat osteoprotegerin (OPG). Anti-OPG  
 CC antibodies can be used in OPG diagnostic assays, and as affinity  
 CC purification materials. The OPG cDNA can be used to express  
 CC recombinant OPG and to generate transgenic animals. It can also  
 CC be used to regulate the level of OPG in mammals, specifically to  
 CC increase OPG levels, however the use of antisense sequences is  
 CC also contemplated. Fragments of the cDNA can be used as probes to  
 CC detect OPG expressing cells and tissue, and to screen cDNA  
 CC libraries for related sequences. OPG can be used to treat or  
 CC prevent bone diseases, specifically excessive bone loss, e.g.  
 CC osteoporosis, Paget's disease, hypercalcaemia,  
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,  
 CC osteolytic metastases, periodontal bone loss, bone necrosis and  
 CC osteopentia.  
 CC  
 XX Sequence 401 AA;  
 SQ  
 Query Match 96.0%; Score 1069; DB 18; Length 401;  
 Best Local Similarity 95.4%; Pred. No. 2,3e-102;  
 Matches 206; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 PY 1 SGNREATORCGIDVTLCCEAFPPFAVPTKIIPNMLSVLYVDSLPCTKVNAESVERIKRRHS 60  
 DB 186 sqnreecgcidvtlceeaftfvaupkllpmlsvlyvdsipgctkvaesverikrrhs 245  
 QY 61 SOEOTFQOLKLMKHONRDQEMVKIIIDIDLCESYORHLGHSNLTTEQLALMESLPK 120  
 DB 246 sqeotfqlklmkhqnrdqemvkkididlcessygrhlgshnltteqlrlmeslpk 305  
 QY 121 KISPEIERTRKTCSSSEQLKLSLWRIKNGDQTLKGLMALKHLKTSHPKTVTHSL 180  
 DB 306 kispelietrtrctckssseqllklslwrkngdqlkglmyalkhlkayhtpkvtshl 365  
 QY 181 RKTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 216  
 DB 366 rktlrlfshftmyrlyqkflflemignovsvkiscsl 401  
 RESULT 4  
 ID W89230 standard; Protein: 208 AA.  
 AC W89230;  
 XX  
 DT 04-MAR-1999 (first entry)  
 DE Rat osteoprotegerin dimerisation domain.  
 XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.

XX  
 OS Rattus sp.  
 XX  
 PN WO9849305-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US08631.  
 XX  
 PR 01-MAY-1997; 97US-0850188.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;  
 DR WPI; 1999-034661/03.  
 DR  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence.  
 PT useful to treat TNF and TNFR-mediated disorders  
 PS  
 XX Disclosure; Fig 1; 92pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents rat OPG dimerisation domain.  
 CC  
 XX Sequence 208 AA;  
 SQ  
 Query Match 92.5%; Score 1029; DB 20; Length 208;  
 Best Local Similarity 95.7%; Pred. No. 1,3e-98;  
 Matches 198; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 10 CGIDVTLCCEAFPPFAVPTKIIPNMLSVLYVDSLPCTKVNAESVERIKRRHSOETK 60  
 DB 2 cgidvtlceeaftfvaupkllpmlsvlyvdsipgctkvaesverikrrhsseqtkl 120  
 QY 70 KLMKHONRDQEMVKIIIDIDLCESYORHLGHSNLTTEQLALMESLPK 120  
 DB 62 klmkhqnrdqemvkkididlcessygrhlgshnltteqlrlmeslpk 305  
 QY 130 TRKTCSSSEQLKLSLWRIKNGDQTLKGLMALKHLKTSHPKTVTHSL 180  
 DB 122 trktckssseqllklslwrkngdqlkglmyalkhlkayhtpkvtshl 365  
 QY 190 FTMYRLYOKLFLEMIGNOVSVKISCL 216  
 DB 182 ftmyrlyqkflflemignovsvkiscsl 408  
 RESULT 5  
 ID R99936 standard; Protein: 360 AA.  
 AC R99936;  
 XX  
 DT 23-APR-1997 (first entry)  
 DE Mutated OCIF, OCIF-DCRI.

KM	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KN	osteoporosis.
XX	
XX	Synthetic.
OS	
FH	Key
FT	Peptide
FT	Protein
FT	Misc-difference
FT	/note= "Signal peptide"
FT	/note= "Mature OCIF-DCR1"
FT	/note= "Position of deletion, delta 2-42"
XX	
XX	
PN	WO9626217-A1.
PD	29-AUG-1996.
XX	
PF	20-FEB-1996; 96MO-JP00374.
XX	
PR	21-JUL-1995; 95JP-0207508.
PR	20-FEB-1995; 95JP-0054977.
PA	(SNOW ) SNOW BRAND MILK PROD CO LTD.
XX	
I	Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
II	Nakagawa N, Shima N, Tsuda E, Ueda W, Yano K, Yasuda H;
DR	WPI; 1996-402320/40.
XX	N-PSDB; T33166.
PT	DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT	for bone resorption control, esp. treatment of osteoporosis
PS	Claim 44; Page 105-107; 183pp; Japanese.
CC	This sequence represents a mutated version of the full length
CC	osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC	sequence represents OCIF-DCR1 in which amino acids 2-42 of the
CC	mature OCIF protein are deleted. The OCIF of the invention
CC	has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
CC	and 120 kD under non-reducing conditions. The protein is adsorbed onto
CC	cation-exchangers or heparin and its activity is lowered after 10 mins
CC	at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC	deg.C. OCIF is useful in the control of bone resorption and therefore
CC	in the treatment and prevention of disorders of bone resorption, e.g.
CC	osteoporosis.
SO	Sequence 360 AA:
	Query Match 87.8%; Score 977; DB 17; Length 360;
	Best Local Similarity 85.2%; Pred.No.6.4e-93;
	Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
Y	1 SCNNREATQCGIDVTLCEAFRRFAPVRKIIPNMLSYLVDSLPGRVNAESVERIKRRHS 60
Db	145 sgnsesgtqcgidvltlceafrrfapvrkiiipnmislvldnlpgrtknaesverikrghs 204
Y	61 SOEORFOLLKLKHONRODEWKRIIIDDLCSSVSORHLGNSNTTTEDLALMESTPECK 120
Db	205 sgeorfollklkhonrodewkriiiddlcssvsorhlgnsttteeblalmestpeck 264
Y	121 KISPEIERTRRTCKSSSEDLKLSLIMRIKNDOPDTLGLMALKHLKTSHPPKVTNLSL 180
Db	265 kygaedietklackpsdqilklslwrlngdgdltlgymalnakhshtyhpktvtgsl 324
Y	181 RRTMRFLHSFTMYRLYOKLELMIGNOVQSVKISC L 216
Db	325 krtfrflhsftmyrklykflemignqvsvkscl 360
RESULT	6
R95924	

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ID R99924 standard; Protein; 380 AA.
XX
AC R99924;
XX
DT 22-APR-1997 (first entry)
XX
DE Mature osteoclastogenesis inhibitory factor.
XX
KM Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
XX
OS Homo sapiens.
XX
PN W09626217-A1.
XX
PD 29-AUG-1996.
XX
PF 20-FEB-1996; 96MO-JP00374.
XX
PR 21-JUL-1995; 95JP-0207508.
XX
PR 20-FEB-1995; 95JP-0054977.
XX
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX
DR WPI; 1996-402320/40.
XX
DR N-PSDB; T36685.
XX
PT DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis
XX
PS Claim 6; Page 62-64; 183pp; Japanese.
XX
CC This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
XX
SQ Sequence 380 AA;
XX
Query Match 87.8%; Score 977; DB 17; Length 380;
Best Local Similarity 85.2%; Pred. No. 6.9e-93;
Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
OY 1 SGNRATQKCGIDVYLCEAFRRFVPRKIIIPNMLSTLYVDSLPRGVAAEVEERIKRHS 60
Db 165 sgnsestqkcgdvdlceeaftfapvprkfpnwslsvdnlpgtkvaeeverikrghs 224
OY 61 SQEQTFQLKLKMHONRPOEMWYKIIIDIDICSSVORHLGHSNLTTEQLALMESLPK 120
Db 225 sqeqtfqlklkwhknkqgdvlvkkidgidicensvqghihantfqlslmeslpk 284
OY 121 KISPEIERTRKTKSSQQLKLKLSLWRKNGDDDTLGLMYALKLTKTSHPPTVTHS 180
Db 285 kvgaedieklackpsdqllklslwlkingddqdlkylmhalkshktyhfpkvtqgs 244
OY 181 RKTMRFLSFTMRKYOKLFLEMIGNOVQKISL 216
Db 345 kktirflnsftmyklygkllflemignqvsvkiscsl 380

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[illegible]

ID	R99925 standard; Protein; 401 AA.
XX	
AC	R99925:
DT	22-APR-1997 (first entry)
XX	
DE	Full length osteoclastogenesis inhibitory factor.
XX	
KW	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resor
KM	osteoporosis.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Protein
FT	Location/Qualifiers 1..21 /note= "Signal peptide" 22..401 /note= "Mature OCIF, claim 6"
XX	
PN	WO9626217-A1.
PD	
XX	
PD	29-AUG-1996.
XX	
PF	20-FEB-1996; 96WO-JP00374.
XX	
PR	21-JUL-1995; 95JP-0207508.
PR	20-FEB-1995; 95JP-0054977.
XX	
PA	(SNOW ) SNOW BRAND MILK PROD CO LTD.
XX	
PI	Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI	Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR	WPI: 1996-402320/40.
DR	N-PADB: T36685.
PT	DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT	for bone resorption control, esp. treatment of osteoporosis
XX	
PS	Disclosure; Page 64-66; 183pp; Japanese.
XX	
CC	This sequence represents the full length osteoclastogenesis inhibitory
CC	factor (OCIF) of the invention. The OCIF has a molecular weight by
CC	SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-
CC	-reducing conditions. The protein is adsorbed onto cation-exchange
CC	resin and its activity is lowered after 10 mins at 70 deg.C, r
CC	30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
CC	useful in the control of bone resorption and therefore in the
CC	treatment and prevention of disorders of bone resorption, e.g.
CC	osteoporosis.
XX	
SQ	Sequence 401 AA;
XX	
Query Match	87.8%; Score 977; DB 17; Length 401;
Best Local Similarity	85.2%; Pred.No. 7.5e-93;
Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;	
QY	1 SGNRRATOKCGIDVYLCEAFRRFVAVPKRIIPNMLSVLYSDSLPGTKVAASEVERIKRRRL
DB	186 sgnstetkcgldvylceeafrfvrpkfpnwslsvlydnlpgetkvaaesverikrrgs 245
QY	61 SOEQFFOLKLWKHHONROEWMVKRIIODIDCESSVORHLGHSNTTBOALLMESLQA 120
DB	246 sqeqffqlklwkhhnknkgdvlkkldidlcemsvqnhghantlfqrlsimesj 5
QY	121 KISPEIERTRKTCKSSBOLLKLSLMWRKMGDDDTLKGLMYALXHLKTSHPKTVTFSS 180
DB	306 kvsgaediekltackpsdqllklslwrikngddgtlkglmalxkskyhpktvtqtal 365
QY	181 RKTMRFLMSFTMYRLYQKLFLEMIGNOVAKYSICL 216
DB	366 ktltirflmsftmyrlyqkflflemignqvskysicl 401

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QY 121 KISEEIEERTEKTSSEBOLKLSIRKINRGDDTLKGLMYALKHLKTSHPKTYVH.
Db 306 kvgeedtektkkaekpsdqjllkllstlrkngddtckglmhalkshktyhfpktyvgs
QY 181 RKTMRPLHSFTMYRLYOKLEPLEMIGNOVOSKVISCL 216
Db 366 KktirfihstfcmYklYgkllflemignvgsvkksl 401

RESULT 10
Y05742 Y05742 standard; Protein; 401 AA.
XX AC Y05742;
XX DT 19-JUL-1999 (first entry)
XX DE Tumour necrosis factor receptor TR1.
XX XX
XX Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist;
XX antagonist; screening; human; cancer; AIDS; Alzheimer's disease;
XX inflammation; arthritis; septicemia; autoimmune disease;
XX psoriasis; inflammatory bowel disease; transplant rejection;
XX graft versus host disease; infection; stroke; ischaemia;
XX acute respiratory disease syndrome; restenosis; brain injury;
XX bone disease; atherosclerosis; therapy.
XX XX
XX Homo sapiens.
XX OS
XX EP911633-A1.
XX PN
XX 28-APR-1999.
XX PD
XX 02-OCT-1998; 98EP-0203332.
XX PF
XX 08-OCT-1997; 97US-0061334.
XX PR
XX (SMIRK ) SMITHKLINE BEECHAM CORP.
XX PA
XX McDonnell PC, Young PR, Zou J;
XX PI
XX WPI; 1999-246560/21.
XX DR
XX
XX Identifying agonists and antagonists of tumor necrosis factor
XX related receptors TR1, TR3 and TR5, and of ligand TL3, useful for
XX treatment of cancer, AIDS, Alzheimer's disease, bone disease etc
XX PT
XX
XX Disclosure; Page 10-12; 23pp; English.
XX PS
XX
XX The present sequence represents tumour necrosis factor receptor
XX CC (TNFR) TR1, also known as osteoprotegerin. The invention relat-
XX CC to TNFR related polypeptides TR1, TR3 and TR5 (see Y05742-44) a-
XX CC their ligand TL3 (see Y05745). TR1, TR3, TR5 and TL3 are used
XX CC claimed methods of identifying agonists and antagonists, i.e.
XX CC compounds that bind to the receptors or ligand, and which activa-
XX CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5
XX CC TL3. A screening kit for identifying agonists, antagonists, li-
XX CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or
XX CC TL3 polypeptides is provided. The agonists and antagonists are
XX CC useful for treatment of chronic and acute inflammation, arthritis,
XX CC septicemia, autoimmune disease e.g. inflammatory bowel disease,
XX CC psoriasis, transplant rejection, graft versus host disease,
XX CC infection, stroke, ischaemia, acute respiratory disease syndrome,
XX CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
XX CC lymphoproliferative disorders), atherosclerosis and Alzheimer's
XX CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.
XX CC
XX Sequence 401 AA;
XX SQ

Query Match 87.88; Score 977; DB 20; Length 401;
Best Local Similarity 85.28; Prid. No. 7, 5e-93;

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XX	Sequence	401 AA:
SO	Query Match	87.8%; Score 977; DB 20; Length 401;
	Best Local Similarity	85.2%; Pred. No. 7.5e-93;
	Matches 184; Conservative	19; Mismatches 13; Indels 0;
OY	1 SGNREATOKCGIDVYLCEAEAFRAVPTRKIIPNMLSVLVDSPGCTRVNAESVERIKRK	100
DB	186 sgnsstqkcgldvrlceaeaffrsvprckfipnwlsvlvdnlpgtkrvnaesverikrgls	245
OY	61 SOEOTFOLLKMKHONRPOENWKITIDIDCESSVQRHLGHNTTTEOLLAMESLPK	120
DB	246 sqegftgllklwkhpnkdqdvkkliqgdldleensvgrnhgnanltfeqlrslneslpk	405
OY	121 KISPEIRRTKTKCKSSFOILLKLISLMFRKNQDQDTLGLMVALMHKTSHPKVTHSI	180
DB	306 kvgaediecltlackpsdqilxlslswtksngddgtlkxglmahalkshsktyhnpkvts	365
OY	181 RKTMRFLHSFTMYRLYQKLFLEMIGNOVOSVKISCL 216	
DB	366 kktlrflhsftmyrklygklflemlgnqvsvkiscsl 401	
RESULT 12		
ID	W83926	
AC	W83926 standard; Protein; 401 AA.	
XX	W83926;	
DT	01-MAR-1999 (first entry)	
XX	Human FTHMA-070 protein.	
DE	FTHMA-070; human; neurological disorder; therapy; diagnosis.	
XX	Homo sapiens.	
OS		
FH	Key	Location/Qualifiers
FT	Peptide	1..21
FT	Protein	/label= Sig-peptide 22..401 /label= Mat_protein
XX	WC9848051-A2.	
PN		
XX	29-OCT-1998.	
PD		
XX	17-APR-1998;	98WO-US07714.
PE		
XX	10-OCT-1997;	97US-0062017.
PR	18-APR-1997;	97US-0044746.
PA	(MTL-) MILLENNIUM BIOTHERAPEUTICS INC.	
XX		
PI	Holtzman D, McCarthy SA;	
XX		
DR	WPI: 1999-024021/02.	
N-PSDB:	V69277.	
PT	New isolated human FTHMA-070 and T85 proteins - used to develop	
PT	products for the diagnosis and therapy of disorders involving	
PT	cellular processes, e.g. neuronal development.	
XX		
PS	Claim 8; Fig 1; 127pp; English.	
CC	This is the amino acid sequence of human FTHMA-070, a novel protein	
CC	having homology to tumor necrosis factor receptor. The sequence	
CC	was deduced from that of a cDNA clone (see V69277) isolated from a	
CC	cardiac coronary artery smooth muscle cell library. FTHMA-070	
CC	nucleic acids and polypeptides of the invention are useful as	
CC	modulating agents in regulating a variety of cellular processes.	

CC They can be used for identifying compounds which bind to or modulate  
 CC the activity of the polypeptides (claimed). They can also be used  
 CC in screening assays, detection assays (e.g. chromosomal mapping,  
 CC tissue typing, forensic biology), predictive medicine (e.g.  
 CC diagnostic assays, prognostic assays, monitoring clinical trials,  
 CC and pharmacogenomics), and methods of treatment (e.g. therapeutic  
 CC and prophylactic) e.g. for neurological disorders.

XX Sequence 401 AA;

SO Query Match 87.8%; Score 977; DB 20; Length 401;

Best Local Similarity 85.2%; Pred. No. 7.5e-93;

Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 SGNREATQCGIDVTLCCEAFRRFVPTKTIIPNLSLVVDSLPQTKVNAESVERIKRRHS 60

DB 186 sgnsestqcgidvtlceeafrfayptkfpnwlsvlvdnpjtkvnaesverikrrhs 245

QY 61 SOEOTFOLLKMKHONRDOEAVKRIIDIDICSSVORHGHSLTTEOLALMESLPK 120

DB 246 sqegtfqlklwkhqkqdvkvkldidicnsygrhghantlfeqlslmeslpk 305

QY 121 KISPEIERTRKTKSSQQLKLSLWIRKNGDDDTLKGMLYALKHUKTSHPKTVHSL 180

DB 306 kvgaedlektlkackpsdqllkllslwrkngddtlkgmlhalkhsktyhfpktvgs 365

QY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216

DB 366 ktirflhsftmyrlyoklflemignovsvkisc 401

RESULT 13

R99937 R99937 standard; Protein; 359 AA.

XX AC R99937;

DT 23-APR-1997 (first entry)

XX DE Mutated OCIF, OCIF-DCR2.

XX KW Osteoclastogenesis inhibitory factor; OCIF, heparin; bone resorption;

XX KM osteoporosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "Signal peptide"

FT Misc-difference 63..64 /note= "Mature OCIF-DCR2"

XX /note= "Position of deletion, delta 43-84"

XX WO9626217-A1.

XX 29-AUG-1996.

XX 20-FEB-1996; 96WO-JP00374.

XX 21-JUL-1995; 95JP-0207508.

XX 20-FEB-1995; 95JP-0054977.

XX (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

XX WPI: 1996-402320/40.

XX N-PSDB: T33167.

PT DNA encoding osteoclastogenesis inhibitory factor protein - useful

PT for bone resorption control, esp. treatment of osteoporosis

XX Claim 47; Page 107-109; 183pp; Japanese.

XX This sequence represents a mutated version of the full length

XX osteoclastogenesis inhibitory factor (OCIF) of the invention.

XX Sequence represents OCIF-DCR2 in which amino acids 43-84 of the

XX mature OCIF protein are deleted. The OCIF of the invention

XX has a molecular weight by SDS-PAGE of 60 kD under reducing conditions

XX and 120 kD under non-reducing conditions. The protein is adsorbed into

XX cation-exchangers or heparin and its activity is lowered after 10 mins

XX at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70

XX deg.C. OCIF is useful in the control of bone resorption and therefore

XX in the treatment and prevention of disorders of bone resorption, e.g.

XX osteoporosis.

XX Sequence 359 AA;

SO Query Match 87.3%; Score 972; DB 17; Length 359;

Best Local Similarity 84.7%; Pred. No. 2.1e-92;

Matches 183; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 SGNREATQCGIDVTLCCEAFRRFVPTKTIIPNLSLVVDSLPQTKVNAESVERIKRRHS 60

DB 144 sgnsestqcgidvtlceeafrfayptkfpnwlsvlvdnpjtkvnaesverikrrhs 203

QY 61 SOEOTFOLLKMKHONRDOEAVKRIIDIDICSSVORHGHSLTTEOLALMESLPK 120

DB 204 sqegtfqlklwkhqkqdvkvkldidicnsygrhghantlfeqlslmeslpk 303

QY 121 KISPEIERTRKTKSSQQLKLSLWIRKNGDDDTLKGMLYALKHUKTSHPKTVHSL 180

DB 264 kvgaedlektlkackpsdqllkllslwrkngddtlkgmlhalkhsktyhfpktvgs 323

QY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216

DB 324 ktirflhsftmyrlyoklflemignovsvkisc 359

RESULT 14

W57635 W57635 standard; Protein; 401 AA.

XX AC W57635;

DT 27-AUG-1998 (first entry)

XX DE TR1 receptor protein.

XX TR1 receptor; tumour necrosis factor receptor-1; TNF-alpha; TNF-related

XX inhibitor; tumour growth; tumour necrosis; microorganism infection;

XX cellular differentiation stimulation; ionising radiation; septic shock;

XX anti-viral response; growth regulator; immune response; meningococemia;

XX AIDS; therapy.

XX Homo sapiens.

XX WO9812344-A1.

XX 26-MAR-1998.

XX 18-SEP-1996; 96WO-US15003.

XX 18-SEP-1996; 96WO-US15003.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fleischmann RD, Greene JM, Ni J;

XX WPI: 1998-217278/19.

XX N-PSDB: V24486.



XX New isolated tumour necrosis factor receptor - useful for developing  
PT products for treating, e.g. tumours, auto-immune disease(s), graft  
PT rejection, apoptosis or inflammation  
XX

Claim 13; Fig 1; 111pp; English.

This sequence is a tumour necrosis factor receptor-1 (TNF-R1) receptor of the invention. The DNA can be used to produce a recombinant host cell by inserting it into a vector, which is then used to transfect the host cell. The TNF-R1 receptor can bind both TNF- $\alpha$  and TNF- $\beta$ . TNF-R1 receptor agonists can be used for inhibition of tumour growth and necrosis of tumours. They can also be used to stimulate cellular differentiation, e.g. T cell, fibroblasts or hematopoietic cell differentiation, may be used to augment TNF-R1's role in the host's defence against microorganisms and prevent related disease. The agonists may also be used to protect against the deleterious effects of ionising radiation produced during a course of radiotherapy, e.g. denaturation of enzymes, lipid peroxidation or DNA damage. The agonists may further be used to mediate an anti-viral response, to regulate growth, to mediate the immune response and to treat immunodeficiencies related to diseases such as HIV. Antagonists to the TNF-R1 receptor may be used to treat autoimmune diseases, e.g. graft versus host rejection and allograft rejection, and T cell mediated autoimmune diseases. They may also be used to prevent apoptosis. They may also be used to prevent cytotoxicity and to treat septic shock, meningococemia, inflammation, bacterial infections, cachexia, cerebral malaria or AIDS. The products can also be used for diagnosing the above diseases.

**SQ**      **Sequence**      **401 AA;**

Query Match	87.3%	Score 972:	DB 19:	Length 401:
Best Local Similarity	84.7%	Pred. No. 2.5e-92:		
Matches 183, Conservative	19:	Mismatches 14:	Indels 0:	Gaps 0

QY	1	SGNRATQKCIDWTLCEAEFFRAVPKIIIPMLSVLVSLOPETKYNASVEIKRRHS	60
Db	186	sgnesckqgldvclceaeffravpkifpnmlsvlvsnlpgckvnaeaverikrghs	245
QY	61	SOEQTFOLLKMKHQNRDOEWKKIIOIDICSSVORHNSMLTTEOLLAMESLPK	120
Db	246	sqeqtfllklmwnkqgdvfkklidgidicensvgrhghnlttegrtlmeslpk	309
QY	121	KISPEEIRTKTKCKSSQQLKLKLSMRKKGDDDTLKGMLYALKHLKTSHFPEKTVHSL	180
Db	306	kvgaediektlckackpsdqllklislswrlkngddctlkglmhalkhekyhfpkiveqsl	365
QY	181	RKTRFLCHSPMYRRLYOKLFLEMIGNOVOSKISCL	216
Db	366	rktrflhstcmvklvqkllflemignqvskiscl	401

RESULT 15  
W38345  
ID W38345 standard; Protein; 401 AA

AC W38345

DT 20-APR-1998 (first entry)

## DE Human osteoprotegerin.

KM Osteopetreggerin: antibody: diagnosis; affinity purification;  
 KM recombinant production; transgenic animal; treatment; prevention;  
 KM antisense oligonucleotide; probe; detection; screening; human;  
 KM bone disease; osteoporosis; Paget's disease; hypercalcaemia;  
 KM hyperparathyroidism; rheumatoid arthritis; osteomyelitis;  
 KM osteolytic metastasis; periodontal bone loss; bone necrosis;  
 KM osteopenia.

OS Homo sapiens.

XX

PN DE19654610-A1

PD 26-JUN-1997.

PF 20-DEC-1996; 96DE-1054610.

PR	03-SEP-1996;	96US-0706945.
PR	03-DEC-1996;	96US-0577780.

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DB WDT: 1007-334371/31

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C]a]m 23. Pages 100-111. 182pp. German  
PS

phs present economies in human cost and effort

The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of antisense sequences is also contemplated. Fragments of the cDNA can be used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or prevent bone diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss, bone necrosis and osteopaenia.

SQ Sequence 401 AA;

Query Match	87.1%	Score 969;	DB 18;	Length 401;
Best Local Similarity	84.7%	Pred. No. 5e-92;		
Matches 183;	Conservative 19;	Mismatches 14;	Indels 0;	Matches 0

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QY 1 SGNEAFOKCIDVTLCEAEFFRAVPKRIIPNMLSVLYSDLPCKTNAEVEVERIKRRH 60
Db 186 sgnsestckgldvllceaeffravpkrfpmlsvlyadlpckvnaeeverikrr 150
QY 61 SOEOTFOLLKMLKQNRDOEKKRIIDIDLCSSVVRHLGNSMLTTEOLLALMESLH 120
Db 246 sqegtfllkhwkqngkagdvkrlkldidlcensvgrhgnhalttegrlsmslpch 300
QY 121 KISPBEIERKTKCKSSQOLLKLKLSMRKKNODDTLKGLMVALKHLKTSHFPRKTVHSI 180
Db 306 kvgaedlektkackpsdqllkllslwrkngddclkgmalhalkhektyfprtvq 360
QY 181 RKTMRFLHSFTMYRLXOKLPLEMIGNOVASKISCL 216
Db 366 kktlrflhsftmyrlyqklflemignovaskiscl 401

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